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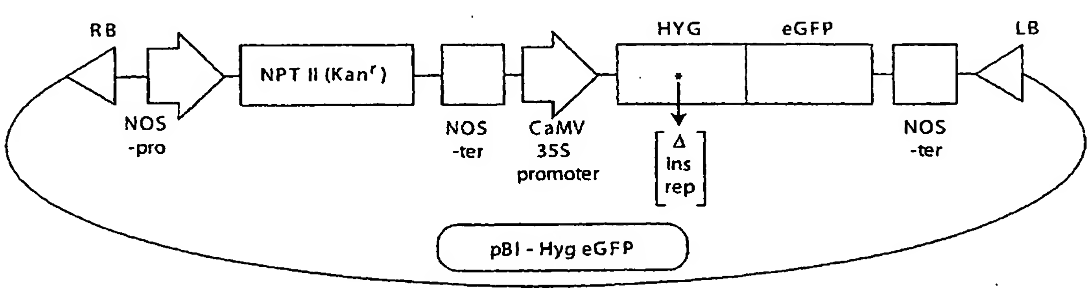
[Continued on next page]

(54) Title: TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES



(57) Abstract: Presented are methods and compositions for targeted chromosomal genomic alterations with modified single-stranded oligonucleotides. The oligonucleotides of the invention have modified nuclease-resisant termini comprising LNA, phosphorothioate linkages or 2'-O-Me base analogues or combinations of such modifications.

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TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

Field Of The Invention

The technical field of the invention is oligonucleotide-directed repair or alteration of plant genetic information using novel chemically modified oligonucleotides.

Background Of The Invention

A number of methods have been developed specifically to alter the genomic information of plants. These methods generally include the use of vectors such as, for example, T-DNA, carrying nucleic acid sequences encoding partial or complete portions of a particular protein which is expressed in a cell or tissue to effect the alteration. The expression of the particular protein then results in the desired phenotype. See, for example, United States Patent 4,459,355 which describes a method for transforming plants with a DNA vector and United States Patent 5,188,642 which describes cloning or expression vectors containing a transgenic DNA sequence which when expressed in plants confers resistance to the herbicide glyphosate. The use of such transgene-containing vectors adds one or more exogenous copies of a gene in a usually random fashion at one or more integration sites of the plant's genome at some variable frequency. The introduced gene may be foreign or may be derived from the host plant. Any gene which was originally present in the genome, which may be, for example, a normal allelic variant, mutated, defective, and/or functional copy of the introduced gene, is retained in the genome of the host plant.

These methods of gene alteration are problematic in that complications which can compromise the vigor, productivity, yield, etc. of the plant may result. One such problem is that insertion of exogenous nucleic acid at random location(s) in the genome can have deleterious effects. The random nature of this insertion and/or the use of exogenous promoters can also cause the timing, location or strength of expression of the introduced transgene to be inappropriate or unpredictable. Another problem with such systems includes the addition of unnecessary and unwanted genetic material to the genome of the recipient, including, for example, T-DNA ends or other vector remnants, exogenous control sequences required to allow production of the transgene protein, which control sequences may be

exogenous or native to the host plant and/or the transgene, and reporter genes or resistance markers. Such remnants and added sequences may have presently unrecognized consequences, for example, involving genetic rearrangements of the recipient genomes. In addition, concerns have been raised with consumption, especially by humans, of plants containing such exogenous genetic material.

More recently, simpler systems involving poly- or oligo- nucleotides have been described for use in the alteration of genomic DNA. These chimeric RNA-DNA oligonucleotides, requiring contiguous RNA and DNA bases in a double-stranded molecule folded by complementarity into a double hairpin conformation, have been shown to effect single basepair or frameshift alterations, for example, for mutation or repair of plant, animal or fungal genomes. See, for example, WO 99/07865 and U.S. Patent 5,565,350. In the chimeric RNA-DNA oligonucleotide, an uninterrupted stretch of DNA bases within the molecule is required for sequence alteration of the targeted genome while the obligate RNA residues are involved in complex stability. Due to the length, backbone composition, and structural configuration of these chimeric RNA-DNA molecules, they are expensive to synthesize and difficult to purify. Moreover, if the RNA-containing strand of the chimeric RNA-DNA oligonucleotide is designed so as to direct gene alteration, a series of mutagenic reactions resulting in nonspecific base alteration can result. Such a result reduces the utility of such a molecule in methods designed for targeted gene alteration.

Alternatively, other oligo- or poly- nucleotides have been used which require a triplex forming, usually polypurine or polypyrimidine, structural domain which binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide. Such oligonucleotides may have an additional DNA reactive moiety, such as psoralen, covalently linked to the oligonucleotide. These reactive moieties function as effective intercalation agents, stabilize the formation of a triplex and can be mutagenic. Such agents may be required in order to stabilize the triplex forming domain of the oligonucleotide with the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Patent 5,422,251. The utility of these oligonucleotides for directing targeted gene alteration is compromised by a high frequency of nonspecific base changes.

In more recent work, the domain for altering a genome is linked or tethered to the triplex forming domain of the bi-functional oligonucleotide, adding an additional linking or tethering functional domain to the oligonucleotide. See, e.g., Culver et al., Nature Biotechnology 17: 989-93 (1999). Such chimeric or triplex forming molecules have distinct structural requirements for each of the different domains of the complete poly- or oligo-nucleotide in order to effect the desired genomic alteration in either episomal or chromosomal targets.

Other genes, e.g. CFTR, have been targeted by homologous recombination using duplex fragments having several hundred basepairs. See, e.g., Kunzelmann et al., Gene Ther. 3:859-867 (1996). Similar efforts to target genes by homologous recombination in plants using large fragments of DNA had some success. See Kempin et al., Nature 389:802-803 (1997). However, the efficiency and reproducibility of the published homologous recombination approach in plants has severely limited the widespread use of this method.

Earlier experiments to mutagenize an antibiotic resistance indicator gene by homologous recombination used an unmodified DNA oligonucleotide rather than larger fragments of DNA, wherein the oligonucleotide had no functional domains other than a region of complementary sequence to the target. See Campbell et al., New Biologist 1: 223-227 (1989). These experiments required large concentrations of the oligonucleotide, exhibited a very low frequency of episomal modification of a targeted exogenous plasmid gene not normally found in the cell and have not been reproduced. However, as shown in examples herein, we have observed that an unmodified DNA oligonucleotide can convert a base at low frequency which is detectable using the assay systems described herein.

Oligonucleotides designed for use in the targeted alteration of genetic information are significantly different from oligonucleotides designed for antisense approaches. For example, antisense oligonucleotides are perfectly complementary to and bind an mRNA strand in order to modify expression of a targeted mRNA and are used at high concentration. As a consequence, they are unable to produce a gene conversion event by either mutagenesis or repair of a defect in the chromosomal DNA of a host genome. Furthermore, the backbone chemical composition used in most oligonucleotides designed for use in antisense approaches renders them inactive as substrates for homologous pairing or mismatch repair enzymes and the high concentrations of oligonucleotide required for antisense applications can be toxic with some types of nucleotide modifications. In addition, antisense oligonucleotides must be complementary to the mRNA and therefore, may not be complementary to the other DNA strand or to genomic sequences that span the junction between intron sequence and exon sequence.

Artificial chromosomes can be useful for the screening purposes identified herein. These molecules are man-made linear or circular DNA molecules constructed from essential cis-acting DNA sequence elements that are responsible for the proper replication and partitioning of natural chromosomes (Murray et al., 1983). The essential elements are: (1) Autonomous Replication Sequences (ARS), (2) Centromeres, and (3) Telomeres.

Yeast artificial chromosomes (YACs) allow large segments of genomic DNA to be cloned and modified (Burke et al., Science 236:806; Peterson et al., Trends Genet. 13:61 (1997); Choi, et al., Nat.

Genet., 4:117-223 (1993), Davies, et al., Biotechnology 11:911-914 (1993), Matsuura, et al., Hum. Mol. Genet., 5:451-459 (1996), Peterson et al., Proc. Natl. Acad. Sci., 93:6605-6609 (1996); and Schedl, et al., Cell, 86:71-82 (1996)). Other vectors also have been developed for the cloning of large segments of genomic DNA, including cosmids, and bacteriophage P1 (Sternberg et al., Proc. Natl. Acad. Sci. U.S.A., 87:103-107 (1990)). YACs have certain advantages over these alternative large capacity cloning vectors (Burke et al., Science, 236:806-812 (1987)). The maximum insert size is 35-30 kb for cosmids, and 100 kb for bacteriophage P1, both of which are much smaller than the maximal insert size for a YAC.

An alternative to YACs are cloning systems based on the *E. coli* fertility factor that have been developed to construct large genomic DNA insert libraries. They are bacterial artificial chromosomes (BACs) and P-1 derived artificial chromosomes (PACs) (Mejia et al., Genome Res. 7:179-186 (1997); Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Ioannou et al., Nat. Genet., 6:84-89 (1994); Hosoda et al., Nucleic Acids Res. 18:3863 (1990)). BACs are based on the *E. coli* fertility plasmid (F factor); and PACs are based on the bacteriophage P1. These vectors propagate at a very low copy number (1-2 per cell) enabling genomic inserts up to 300 kb in size to be stably maintained in recombination deficient hosts. The PACs and BACs are circular DNA molecules that are readily isolated from the host genomic background by classical alkaline lysis (Birnboim et al., Nucleic Acids Res. 7:1513-1523 (1979)). In addition, BACs have been developed for transformation of plants with high-molecular weight DNA using the T-DNA system (Hamilton, Gene 24:107-116 (1997); Frary & Hamilton, Transgenic Res. 10: 121-132 (2001)).

A need exists for simple, inexpensive oligonucleotides capable of producing targeted alteration of genetic material such as those described herein as well as methods to identify optimal oligonucleotides that accurately and efficiently alter target DNA.

Summary Of The Invention

Novel, modified single-stranded nucleic acid molecules that direct gene alteration in plants are identified and the efficiency of alteration is analyzed both *in vitro* using a cell-free extract assay and *in vivo* using a yeast system and a plant system. The alteration in an oligonucleotide of the invention may comprise an insertion, deletion, substitution, as well as any combination of these. Site specific alteration of DNA is not only useful for studying function of proteins *in vivo*, but it is also useful for creating plants with desired phenotypes, including, for example, environmental stress tolerance, improved nutritional value, herbicide resistance, disease resistance, modified oil production, modified starch production, and altered floral morphology including selective sterility. As described herein,

oligonucleotides of the invention target directed specific gene alterations in genomic double-stranded DNA in cells. The target genomic DNA can be nuclear chromosomal DNA as well as plastid or mitochondrial chromosomal DNA. The target DNA can also be a transgene present in the plant cell, including; for example, a previously introduced T-DNA. For screening purposes, the target plant DNA can also be extrachromosomal DNA present in plant or non-plant cells in various forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), as well as episomal DNA, including episomal DNA from an exogenous source such as a plasmid or recombinant vector. Many of these artificial chromosome constructs containing plant DNA can be obtained from a variety of sources, including, e.g., the Arabidopsis Biological Resource Center (ABRC) at the Ohio State University, and the Rice Genome Research Program at the MAFF DNA bank in Ibaraki, Japan. The target DNA may be transcriptionally silent or active. In a preferred embodiment, the target DNA to be altered is the non-transcribed strand of a genomic DNA duplex. In a more preferred embodiment, the target DNA to be altered is the non-transcribed strand of a transcribed gene of a genomic DNA duplex.

The low efficiency of targeted gene alteration obtained using unmodified DNA oligonucleotides is believed to be largely the result of degradation by nucleases present in the reaction mixture or the target cell. Although different modifications are known to have different effects on the nuclease resistance of oligonucleotides or stability of duplexes formed by such oligonucleotides (see, e.g., Koshkin et al., J. Am. Chem. Soc., 120:13252-3), we have found that it is not possible to predict which of any particular known modification would be most useful for any given alteration event, including for the construction of gene alteration oligonucleotides, because of the interaction of different as yet unidentified proteins during the gene alteration event. Herein, a variety of nucleic acid analogs have been developed that increase the nuclease resistance of oligonucleotides that contain them, including, e.g., nucleotides containing phosphorothioate linkages or 2'-O-methyl analogs. We recently discovered that single-stranded DNA oligonucleotides modified to contain 2'-O-methyl RNA nucleotides or phosphorothioate linkages can enable specific alteration of genetic information at a higher level than either unmodified single-stranded DNA or a chimeric RNA/DNA molecule. See, for example, copending applications United States application no. 60/208,538, United States application no. 60/244,989, United States application no. 09/818,875, international application no. PCT/US01/09761 and Gamper et al., Nucleic Acids Research 28: 4332-4339 (2000), the disclosures of which are incorporated herein in their entirety by reference. We also found that additional nucleic acid analogs which increase the nuclease resistance of oligonucleotides that contain them, including, e.g., "locked nucleic acids" or "LNAs", xylo-

LNAs and L-ribo-LNAs; see, for example, Wengel & Nielsen, WO 99/14226; Wengel, WO 00/56748; Wengel, WO 00/66604; and Jakobsen & Koshkin, WO 01/25478 also allow specific targeted alteration of genetic information.

The assay allows for determining the optimum length of the oligonucleotide, optimum sequence of the oligonucleotide, optimum position of the mismatched base or bases, optimum chemical modification or modifications, optimum strand targeted for identifying and selecting the most efficient oligonucleotide for a particular gene alteration event by comparing to a control oligonucleotide. Control oligonucleotides may include a chimeric RNA-DNA double hairpin oligonucleotide directing the same gene alteration event, an oligonucleotide that matches its target completely, an oligonucleotide in which all linkages are phosphorothiolated, an oligonucleotide fully substituted with 2'-O-methyl analogs or an RNA oligonucleotide. Such control oligonucleotides either fail to direct a targeted alteration or do so at a lower efficiency as compared to the oligonucleotides of the invention. The assay further allows for determining the optimum position of a gene alteration event within an oligonucleotide, optimum concentration of the selected oligonucleotide for maximum alteration efficiency by systematically testing a range of concentrations, as well as optimization of either the source of cell extract by testing different plants or strains, or testing cells derived from different plants or strains, or plant cell lines. Using a series of single-stranded oligonucleotides, comprising all RNA or DNA residues and various mixtures of the two, several new structures are identified as viable molecules in nucleotide conversion to direct or repair a genomic mutagenic event. When extracts from mammalian, plant and fungal cells are used and are analyzed using a genetic readout assay in bacteria, single-stranded oligonucleotides having one of several modifications are found to be more active than a control RNA-DNA double hairpin chimera structure when evaluated using an *in vitro* gene repair assay. Similar results are also observed *in vivo* using yeast, mammalian and plant cells. Molecules containing various lengths of modified bases were found to possess greater activity than unmodified single-stranded DNA molecules.

Detailed Description Of The Invention

The present invention provides oligonucleotides having chemically modified, nuclease resistant residues, preferably at or near the termini of the oligonucleotides, and methods for their identification and use in targeted alteration of plant genetic material, including gene mutation, targeted gene repair and gene knockout. The oligonucleotides are preferably used for mismatch repair or alteration by changing at least one nucleic acid base, or for frameshift repair or alteration by addition or deletion of at least one nucleic acid base. The oligonucleotides of the invention direct any such alteration,

including gene correction, gene repair or gene mutation and can be used, for example, to introduce a polymorphism or haplotype or to eliminate ("knockout") a particular protein activity. For example, gene alterations that knockout a particular protein activity can be obtained using oligonucleotides designed to convert a codon in the coding region of the protein to a stop codon, thus prematurely terminating translation of the protein. Oligonucleotides that introduce stop codons in the open-reading-frame of the protein are one embodiment of the invention. Generally, oligonucleotides that introduce stop codons early in the open-reading-frame of the protein are preferred. If the open-reading-frame contains more than one methionine, oligonucleotides that introduce stop codons after the second methionine are preferred. Additionally, if the gene exhibits alternative splice sites, oligonucleotides that introduce stop codons in exons after the alternative splice site are preferred. The following table provides examples of codons that can be converted to stop codons by altering a single oligonucleotide. A skilled artisan could readily identify other codons that can be converted to stop codons by altering one, two or three of the base pairs in a given codon. Similarly, a skilled artisan could readily identify codons that can be converted to stop codons by a frameshift mutations that inserts or deletes one or two base pairs in the open-reading-frame. It is also understood that more than one stop codon can be generated in a single open-reading-frame and that these stop codons can be adjacent in the sequence or separated by intervening codons. Where more than one stop codon is introduced into a single open-reading-frame, such alterations can be generated by a single or multiple oligonucleotides and can be generated simultaneously or by sequential mutagenesis of the target nucleic acid.

Original codons*	Corresponding stop codon
GGA (glycine), **A**GA (arginine), **C**GA (arginine), T**T**A (leucine), T**C**A (serine), TG**T** (cysteine), TG**G** (tryptophan), TG**C** (cysteine)	TGA
AAG (lysine), **G**AG (glutamate), **C**AG (glutamine), T**T**G (leucine), T**C**G (serine), T**G**G (tryptophan), TA**T** (cysteine), TA**C** (tyrosine)	TAG
AAA (lysine), **G**AA (glutamate), **C**AA (glutamine), T**T**A (leucine), T**C**A (serine), TA**T** (cysteine), TA**C** (tyrosine)	TAA

*The amino acid encoded by the original codon is shown in parentheses and the base targeted for alteration to convert the codon to the corresponding stop codon is underlined and in bold

The oligonucleotides of the invention are designed as substrates for homologous pairing and repair enzymes and as such have a unique backbone composition that differs from chimeric RNA-DNA double hairpin oligonucleotides, antisense oligonucleotides, and/or other poly- or oligo-nucleotides used for altering genomic DNA, such as triplex forming oligonucleotides. The single-stranded oligonucleotides described herein are inexpensive to synthesize and easy to purify. In side-by-side comparisons, an optimized single-stranded oligonucleotide comprising modified residues as described herein is significantly more efficient than a chimeric RNA-DNA double hairpin oligonucleotide in directing a base substitution or frameshift mutation in a cell-free extract assay.

We have discovered that single-stranded oligonucleotides having a DNA domain surrounding the targeted base, with the domain preferably central to the poly- or oligo-nucleotide, and having at least one modified end, preferably at the 3' terminal region, are able to alter a target genetic sequence and with an efficiency that is higher than chimeric RNA-DNA double hairpin oligonucleotides disclosed in US Patent 5,565,350. Preferred oligonucleotides of the invention have at least two modified bases on at least one of the termini, preferably the 3' terminus of the oligonucleotide. Oligonucleotides of the invention can efficiently be used to introduce targeted alterations in a genetic sequence of DNA in the presence of human, animal, plant, fungal (including yeast) proteins and in cells of different types including, for example, plant cells, fungal cells including *S. cerevisiae*, *Ustillago maydis*, *Candida albicans*, and mammalian cells. Particularly preferred are cells and cell extracts derived from plants including, for example, experimental model plants such as *Chlamydomonas reinhardtii*, *Physcomitrella patens*, and *Arabidopsis thaliana* in addition to crop plants such as cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), fruits such as apples (*Malus*, e.g. *domesticus*), mangoes (*Mangifera*, e.g. *indica*), banana (*Musa*, e.g. *acuminata*), berries (such as currant, *Ribes*, e.g. *rubrum*), kiwifruit (*Actinidia*, e.g. *chinensis*), grapes (*Vitis*, e.g. *vinifera*), bell peppers (*Capsicum*, e.g. *annuum*), cherries (such as the sweet cherry, *Prunus*, e.g. *avium*), cucumber (*Cucumis*, e.g. *sativus*), melons (*Cucumis*, e.g. *melo*), nuts (such as walnut, *Juglans*, e.g. *regia*; peanut, *Arachis hypogeae*), orange (*Citrus*, e.g. *maxima*), peach (*Prunus*, e.g. *persica*), pear (*Pyra*, e.g. *communis*), plum (*Prunus*, e.g. *domestica*), strawberry (*Fragaria*, e.g. *moschata* or *vesca*), tomato (*Lycopersicon*, e.g. *esculentum*); leaves and forage, such as alfalfa (*Medicago*, e.g. *sativa* or *truncatula*), cabbage (e.g. *Brassica oleracea*), endive (*Cichoreum*, e.g. *endivia*), leek (*Allium*, e.g. *porrum*), lettuce (*Lactuca*, e.g. *sativa*), spinach (*Spinacia*, e.g. *oleraceae*), tobacco (*Nicotiana*, e.g. *tabacum*); roots, such as arrowroot (*Maranta*, e.g. *arundinacea*), beet (*Beta*, e.g. *vulgaris*), carrot (*Daucus*, e.g. *carota*), cassava (*Manihot*, e.g. *esculenta*), turnip (*Brassica*, e.g. *rapa*), radish (*Raphanus*, e.g. *sativus*), yam (*Dioscorea*, e.g. *esculenta*), sweet potato (*Ipomoea batatas*); seeds, including oilseeds,

such as beans (*Phaseolus*, e.g. *vulgaris*), pea (*Pisum*, e.g. *sativum*), soybean (*Glycine*, e.g. *max*), cowpea (*Vigna unguiculata*), mothbean (*Vigna aconitifolia*), wheat (*Triticum*, e.g. *aestivum*), sorghum (*Sorghum* e.g. *bicolor*), barley (*Hordeum*, e.g. *vulgare*), corn (*Zea*, e.g. *mays*), rice (*Oryza*, e.g. *sativa*), rapeseed (*Brassica napus*), millet (*Panicum* sp.), sunflower (*Helianthus annuus*), oats (*Avena sativa*), chickpea (*Cicer*, e.g. *arietinum*); tubers, such as kohlrabi (*Brassica*, e.g. *oleraceae*), potato (*Solanum*, e.g. *tuberosum*) and the like; fiber and wood plants, such as flax (*Linum* e.g. *usitatissimum*), cotton (*Gossypium* e.g. *hirsutum*), pine (*Pinus* sp.), oak (*Quercus* sp.), eucalyptus (*Eucalyptus* sp.), and the like and ornamental plants such as turfgrass (*Lolium*, e.g. *rigidum*), petunia (*Petunia*, e.g. x *hybrida*), hyacinth (*Hyacinthus orientalis*), carnation (*Dianthus* e.g. *caryophyllus*), delphinium (*Delphinium*, e.g. *ajacis*), Job's tears (*Coix lacryma-jobi*), snapdragon (*Antirrhinum majus*), poppy (*Papaver*, e.g. *nudicaule*), lilac (*Syringa*, e.g. *vulgaris*), hydrangea (*Hydrangea* e.g. *macrophylla*), roses (including Gallicas, Albas, Damasks, Damask Perpetuals, Centifolias, Chinas, Teas and Hybrid Teas) and ornamental goldenrods (e.g. *Solidago* spp.). Such plant cells can then be used to regenerate whole plants according to methods described herein or any method known in the art. The DNA domain of the oligonucleotides is preferably fully complementary to one strand of the gene target, except for the mismatch base or bases responsible for the gene alteration event(s). On either side of the preferably central DNA domain, the contiguous bases may be either RNA bases or, preferably, are primarily DNA bases. The central DNA domain is generally at least 8 nucleotides in length. The base(s) targeted for alteration in the most preferred embodiments are at least about 8, 9 or 10 bases from one end of the oligonucleotide.

According to certain embodiments, one or both of the termini of the oligonucleotides of the present invention comprise phosphorothioate modifications, LNA backbone (including LNA derivatives and analogs) modifications, or 2'-O-methyl base analogs, or any combination of these modifications. Oligonucleotides comprising 2'-O-methyl or LNA analogs are a mixed DNA/RNA polymer. The oligonucleotides of the invention are, however, single-stranded and are not designed to form a stable internal duplex structure within the oligonucleotide. The efficiency of gene alteration is surprisingly increased with oligonucleotides having internal complementary sequence comprising phosphorothioate modified bases as compared to 2'-O-methyl modifications. This result indicates that specific chemical interactions are involved between the converting oligonucleotide and the proteins involved in the conversion. The effect of other such chemical interactions to produce nuclease resistant termini using modifications other than LNA (including LNA derivatives or analogs), phosphorothioate linkages, or 2'-O-methyl analog incorporation into an oligonucleotide can not yet be predicted because the proteins

involved in the alteration process and their particular chemical interaction with the oligonucleotide substituents are not yet known and cannot be predicted.

In the examples, oligonucleotides of defined sequence are provided for alteration of genes in particular plants. Provided the teachings of the instant application, one of skill in the art could readily design oligonucleotides to introduce analogous alterations in homologous genes from any plant. Furthermore, in the tables of these examples, the oligonucleotides of the invention are not limited to the particular sequences disclosed. The oligonucleotides of the invention include extensions of the appropriate sequence of the longer 120 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Thus the oligonucleotides of the invention include for each correcting change, oligonucleotides of length 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. In some embodiments, longer nucleic acids of up to 240 bases which comprise the sequences disclosed herein may be used. Moreover, the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides of the invention as disclosed in the various tables for alteration of particular plant genes contain phosphorothioate linkages, 2'-O-methyl analog or LNA (including LNA derivatives and analogs) or any combination of these modifications just as the assay oligonucleotides do.

The present invention, however, is not limited to oligonucleotides that contain any particular nuclease resistant modification. Oligonucleotides of the invention may be altered with any combination of additional LNAs (including LNA derivatives and analogs), phosphorothioate linkages or 2'-O-methyl analogs to maximize conversion efficiency. For oligonucleotides of the invention that are longer than about 17 to about 25 bases in length, internal as well as terminal region segments of the backbone may be altered. Alternatively, simple fold-back structures at each end of a oligonucleotide or appended end groups may be used in addition to a modified backbone for conferring additional nuclease resistance.

The different oligonucleotides of the present invention preferably contain more than one of the aforementioned backbone modifications at each end. In some embodiments, the backbone modifications are adjacent to one another. However, the optimal number and placement of backbone modifications for any individual oligonucleotide will vary with the length of the oligonucleotide and the particular type of backbone modification(s) that are used. If constructs of identical sequence having

phosphorothioate linkages are compared, 2, 3, 4, 5, or 6 phosphorothioate linkages at each end are preferred. If constructs of identical sequence having 2'-O-methyl base analogs are compared, 1, 2, 3 or 4 analogs are preferred. The optimal number and type of backbone modifications for any particular oligonucleotide useful for altering target DNA may be determined empirically by comparing the alteration efficiency of the oligonucleotide comprising any combination of the modifications to a control molecule of comparable sequence using any of the assays described herein. The optimal position(s) for oligonucleotide modifications for a maximally efficient altering oligonucleotide can be determined by testing the various modifications as compared to control molecule of comparable sequence in one of the assays disclosed herein. In such assays, a control molecule includes, e.g., a completely 2'-O-methyl substituted molecule, a completely complementary oligonucleotide, or a chimeric RNA-DNA double hairpin.

Increasing the number of phosphorothioate linkages, LNAs or 2'-O-methyl bases beyond the preferred number generally decreases the gene repair activity of a 25 nucleotide long oligonucleotide. Based on analysis of the concentration of oligonucleotide present in the extract after different time periods of incubation, it is believed that the terminal modifications impart nuclease resistance to the oligonucleotide thereby allowing it to survive within the cellular environment. However, this may not be the only possible mechanism by which such modifications confer greater efficiency of conversion. For example, as disclosed herein, certain modifications to oligonucleotides confer a greater improvement to the efficiency of conversion than other modifications.

Efficiency of conversion is defined herein as the percentage of recovered substrate molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. the genome of a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be sequenced to determine the percentage that have acquired the desire change. The oligonucleotides of the invention in different embodiments can alter DNA two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold more than control oligonucleotides. Such control oligonucleotides are oligonucleotides with fully phosphorothiolated linkages, oligonucleotides that are fully substituted with 2'-O-methyl analogs, a perfectly matched oligonucleotide that is fully complementary to a target sequence or a chimeric DNA-RNA double hairpin oligonucleotide such as disclosed in US Patent 5,565,350.

In addition, for a given oligonucleotide length, additional modifications interfere with the ability of the oligonucleotide to act in concert with the cellular recombination or repair enzyme machinery

which is necessary and required to mediate a targeted substitution, addition or deletion event in DNA. For example, fully phosphorothiolated or fully 2-O-methylated molecules are inefficient in targeted gene alteration.

The oligonucleotides of the invention as optimized for the purpose of targeted alteration of genetic material, including gene knockout or repair, are different in structure from antisense oligonucleotides that may possess a similar mixed chemical composition backbone. The oligonucleotides of the invention differ from such antisense oligonucleotides in chemical composition, structure, sequence, and in their ability to alter genomic DNA. Significantly, antisense oligonucleotides fail to direct targeted gene alteration. The oligonucleotides of the invention may target either strand of DNA and can include any component of the genome including, for example, intron and exon sequences. The preferred embodiment of the invention is a modified oligonucleotide that binds to the non-transcribed strand of a genomic DNA duplex. In other words, the preferred oligonucleotides of the invention target the sense strand of the DNA, i.e. the oligonucleotides of the invention are complementary to the non-transcribed strand of the target duplex DNA. The sequence of the non-transcribed strand of a DNA duplex is found in the mRNA produced from that duplex, given that mRNA uses uracil-containing nucleotides in place of thymine-containing nucleotides.

Moreover, the initial observation that single-stranded oligonucleotides comprising these modifications and lacking any particular triplex forming domain have reproducibly enhanced gene alteration activity in a variety of assay systems as compared to a chimeric RNA-DNA double-stranded hairpin control or single-stranded oligonucleotides comprising other backbone modifications was surprising. The single-stranded molecules of the invention totally lack the complementary RNA binding structure that stabilizes a normal chimeric double-stranded hairpin of the type disclosed in U.S. Patent 5,565,350 yet is more effective in producing targeted base conversion as compared to such a chimeric RNA-DNA double-stranded hairpin. In addition, the molecules of the invention lack any particular triplex forming domain involved in Hoogsteen interactions with the DNA double helix and required by other known oligonucleotides in other oligonucleotide-dependant gene conversion systems. Although the lack of these functional domains was expected to decrease the efficiency of an alteration in a sequence, just the opposite occurs: the efficiency of sequence alteration using the modified oligonucleotides of the invention is higher than the efficiency of sequence alteration using a chimeric RNA-DNA hairpin targeting the same sequence alteration. Moreover, the efficiency of sequence alteration or gene conversion directed by an unmodified oligonucleotide is many times lower as compared to a control chimeric RNA-DNA molecule or the modified oligonucleotides of the invention targeting the

same sequence alteration. Similarly, molecules containing at least 3 2'-O-methyl base analogs are about four to five fold less efficient as compared to an oligonucleotide having the same number of phosphorothioate linkages.

The oligonucleotides of the present invention for alteration of a single base are about 17 to about 121 nucleotides in length, preferably about 17 to about 74 nucleotides in length. Most preferably, however, the oligonucleotides of the present invention are at least about 25 bases in length, unless there are self-dimerization structures within the oligonucleotide. If the oligonucleotide has such an unfavorable structure, lengths longer than 35 bases are preferred. Oligonucleotides with modified ends both shorter and longer than certain of the exemplified, modified oligonucleotides herein function as gene repair or gene knockout agents and are within the scope of the present invention.

Once an oligomer is chosen, it can be tested for its tendency to self-dimerize, since self-dimerization may result in reduced efficiency of alteration of genetic information. Checking for self-dimerization tendency can be accomplished manually or, preferably, using a software program. One such program is Oligo Analyzer 2.0, available through Integrated DNA Technologies (Coralville, IA 52241) (http://www.idtdna.com); this program is available for use on the world wide web at

http://www.idtdna.com/program/oligoanalyzer/
oligoanalyzer.asp.

For each oligonucleotide sequence input into the program, Oligo Analyzer 2.0 reports possible self-dimerized duplex forms, which are usually only partially duplexed, along with the free energy change associated with such self-dimerization. Delta G-values that are negative and large in magnitude, indicating strong self-dimerization potential, are automatically flagged by the software as "bad". Another software program that analyzes oligomers for pair dimer formation is Primer Select from DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715, Phone: (608) 258-7420 (http://www.dnastar.com/products/PrimerSelect.html).

If the sequence is subject to significant self-dimerization, the addition of further sequence flanking the "repair" nucleotide can improve gene correction frequency.

Generally, the oligonucleotides of the present invention are identical in sequence to one strand of the target DNA, which can be either strand of the target DNA, with the exception of one or more targeted bases positioned within the DNA domain of the oligonucleotide, and preferably toward the middle between the modified terminal regions. Preferably, the difference in sequence of the oligonucleotide as compared to the targeted genomic DNA is located at about the middle of the oligonucleotide sequence. In a preferred embodiment, the oligonucleotides of the invention are complementary to the non-transcribed

strand of a duplex. In other words, the preferred oligonucleotides target the sense strand of the DNA, i.e. the oligonucleotides of the invention are preferably complementary to the strand of the target DNA the sequence of which is found in the mRNA.

The oligonucleotides of the invention can include more than a single base change. In an oligonucleotide that is about a 70-mer, with at least one modified residue incorporated on the ends, as disclosed herein, multiple bases can be simultaneously targeted for change. The target bases may be up to 27 nucleotides apart and may not be changed together in all resultant plasmids in all cases. There is a frequency distribution such that the closer the target bases are to each other in the central DNA domain within the oligonucleotides of the invention, the higher the frequency of change in a given cell. Target bases only two nucleotides apart are changed together in every case that has been analyzed. The farther apart the two target bases are, the less frequent the simultaneous change. Thus, oligonucleotides of the invention may be used to repair or alter multiple bases rather than just one single base. For example, in a 74-mer oligonucleotide having a central base targeted for change, a base change event up to about 27 nucleotides away can also be effected. The positions of the altering bases within the oligonucleotide can be optimized using any one of the assays described herein. Preferably, the altering bases are at least about 8 nucleotides from one end of the oligonucleotide.

The oligonucleotides of the present invention can be introduced into cells by any suitable means. According to certain preferred embodiments, the modified oligonucleotides may be used alone. Suitable means, however, include the use of polycations, cationic lipids, liposomes, polyethylenimine (PEI), electroporation, biolistics, microinjection and other methods known in the art to facilitate cellular uptake. For plant cells, biolistic or particle bombardment methods are typically used. According to certain preferred embodiments of the present invention, isolated plant cells are treated in culture according to the methods of the invention, to mutate or repair a target gene. Alternatively, plant target DNA may be modified *in vitro* or in another cell type, including for example, yeast or bacterial cells and then introduced into a plant cell as, for example, a T-DNA. Plant cells thus modified may be used to regenerate the whole organism as, for example, in a plant having a desired targeted genomic change. In other instances, targeted genomic alteration, including repair or mutagenesis, may take place *in vivo* following direct administration of the modified, single-stranded oligonucleotides of the invention to a subject.

The single-stranded, modified oligonucleotides of the present invention have numerous applications as gene repair, gene modification, or gene knockout agents. Such oligonucleotides may be advantageously used, for example, to introduce or correct multiple point mutations. Each mutation leads to the addition, deletion or substitution of at least one base pair. The methods of the present invention

offer distinct advantages over other methods of altering the genetic makeup of an organism, in that only the individually targeted bases are altered. No additional foreign DNA sequences are added to the genetic complement of the organism. Such agents may, for example, be used to develop plants with improved traits by rationally changing the sequence of selected genes in isolated cells and using these modified cells to regenerate whole plants having the altered gene. See, e.g., U.S. Patent 6,046,380 and U.S. Patent 5,905,185 incorporated herein by reference. Such plants produced using the compositions of the invention lack additional undesirable selectable markers or other foreign DNA sequences. Targeted base pair substitution or frameshift mutations introduced by an oligonucleotide in the presence of a cell-free extract also provides a way to modify the sequence of extrachromosomal elements, including, for example, plasmids, cosmids and artificial chromosomes. The oligonucleotides of the invention also simplify the production of plants having particular modified or inactivated genes. Altered plant model systems such as those produced using the methods and oligonucleotides of the invention are invaluable in determining the function of a gene and in evaluating drugs. The oligonucleotides and methods of the present invention may also be used to introduce molecular markers, including, for example, SNPs, RFLPs, AFLPs and CAPs.

The purified oligonucleotide compositions may be formulated in accordance with routine procedures depending on the target. For example, purified oligonucleotide can be used directly in a standard reaction mixture to introduce alterations into targeted DNA *in vitro* or where cells are the target as a composition adapted for bathing cells in culture or for microinjection into cells in culture. The purified oligonucleotide compositions may also be provided on coated microbeads for biolistic delivery into plant cells. Where necessary, the composition may also include a solubilizing agent. Generally, the ingredients will be supplied either separately or mixed together in single-use form, for example, as a dry, lyophilized powder or water-free concentrate. In general, dosage required for efficient targeted gene alteration will range from about 0.001 to 50,000 μg/kg target tissue, preferably between 1 to 250 μg/kg, and most preferably at a concentration of between 30 and 60 micromolar.

For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In a preferred method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim) or an equivalent such as lipofectin. The amount of the oligonucleotide used is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells. For electroporation, between 20 and 2000 nanograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve

efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein. For biolistic delivery, microbeads are generally coated with resuspended oligonucleotides, which range of oligonucleotide to microbead concentration can be similarly adjusted to improve efficiency as determined using one of the assay methods described herein, starting with about 0.05 to 1 microgram of oligonucleotide to 25 microgram of 1.0 micrometer gold beads or similar microcarrier.

Another aspect of the invention is a kit comprising at least one oligonucleotide of the invention. The kit may comprise an additional reagent or article of manufacture. The additional reagent or article of manufacture may comprise a delivery mechanism, cell extract, a cell, or a plasmid, such as one of those disclosed in the Figures herein, for use in an assay of the invention. Alternatively, the invention includes a kit comprising an isogenic set of cells in which each cell in the kit comprises a different altered amino acid for a target protein encoded by a targeted altered gene within the cell produced according to the methods of the invention.

Brief Description Of The Drawings

Figure 1. *Flow diagram for the generation of modified single-stranded oligonucleotides.* The upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (A) 2'-O-methyl RNA nucleotides or (B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. HUH7 cells are described in Nakabayashi et al., Cancer Research 42: 3858-3863 (1982). Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene. The numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the molecule. Hence oligo 12S/25G contains an all phosphorothioate backbone, displayed as a dotted line. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G). Figure 1(C) provides a schematic plasmid indicating the sequence of the kan chimeric double-stranded hairpin oligonucleotide (left) and the sequence the tet chimeric double-stranded hairpin oligonucleotide used in other experiments. Figure 1(D) provides a flow chart of a kan experiment in which a chimeric double-stranded hairpin oligonucleotide is used.

Figure 2. *Genetic readout system for correction of a point mutation in plasmid* pK^sm4021. A mutant kanamycin gene harbored in plasmid pK^sm4021 is the target for correction by oligonucleotides.

The mutant G is converted to a C by the action of the oligo. Corrected plasmids confer resistance to kanamycin in *E.coli* (DH10B) after electroporation leading to the genetic readout and colony counts.

Figure 3: *Target plasmid and sequence correction of a frameshift mutation by chimeric and single-stranded oligonucleotides.* (A) Plasmid $pT^s\Delta208$ contains a single base deletion mutation at position 208 rendering it unable to confer tet resistance. The target sequence presented below indicates the insertion of a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) DNA sequence confirming base insertion directed by Tet 3S/25G; the yellow highlight indicates the position of frameshift repair.

Figure 4. *DNA sequences of representative kan^r colonies.* Confirmation of sequence alteration directed by the indicated molecule is presented along with a table outlining codon distribution. Note that 10S/25G and 12S/25G elicit both mixed and unfaithful gene repair. The number of clones sequenced is listed in parentheses next to the designation for the single-stranded oligonucleotide. A plus (+) symbol indicates the codon identified while a figure after the (+) symbol indicates the number of colonies with a particular sequence. TAC/TAG indicates a mixed peak. Representative DNA sequences are presented below the table with yellow highlighting altered residues.

Figure 5. *Gene correction in HeLa cells.* Representative oligonucleotides of the invention are co-transfected with the pCMVneo(-)FlAsH plasmid (shown in Figure 9) into HeLa cells. Ligand is diffused into cells after co-transfection of plasmid and oligonucleotides. Green fluorescence indicates gene correction of the mutation in the antibiotic resistance gene. Correction of the mutation results in the expression of a fusion protein that carries a marker ligand binding site and when the fusion protein binds the ligand, a green fluorescence is emitted. The ligand is produced by Aurora Biosciences and can readily diffuse into cells enabling a measurement of corrected protein function; the protein must bind the ligand directly to induce fluorescence. Hence cells bearing the corrected plasmid gene appear green while "uncorrected" cells remain colorless.

Figure 6. *Z-series imaging of corrected cells.* Serial cross-sections of the HeLa cell represented in Figure 5 are produced by Zeiss 510 LSM confocal microscope revealing that the fusion protein is contained within the cell.

Figure 7. *Hygromycin-eGFP target plasmids.* (A) Plasmid pAURHYG(ins)GFP contains a single base insertion mutation between nucleotides 136 and 137, at codon 46, of the Hygromycin B coding sequence (cds) which is transcribed from the constitutive ADH1 promoter. The target sequence presented below indicates the deletion of an A and the substitution of a C for a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) Plasmid pAURHYG(rep)GFP contains a

base substitution mutation introducing a G at nucleotide 137, at codon 46, of the Hygromycin B coding sequence (cds). The target sequence presented below the diagram indicates the amino acid conservative replacement of G with C, restoring gene function.

Figure 8. *Oligonucleotides for correction of hygromycin resistance gene.* The sequence of the oligonucleotides used in experiments to assay correction of a hygromycin resistance gene are shown. DNA residues are shown in capital letters, RNA residues are shown in lowercase and nucleotides with a phosphorothioate backbone are capitalized and underlined.

Figure 9. *pAURNeo(-)FlAsH plasmid.* This figure describes the plasmid structure, target sequence, oligonucleotides, and the basis for detection of the gene alteration event by fluorescence.

Figure 10. pYESHyg(x)eGFP plasmid. This plasmid is a construct similar to the pAURHyg(x)eGFP construct shown in Figure 7, except the promoter is the inducible GAL1 promoter. This promoter is inducible with galactose, leaky in the presence of raffinose, and repressed in the presence of dextrose.

Figure 11. pBI-HygeGFP plasmid. This plasmid is a construct based on the plasmids pBI101, pBI 101.2, pBI101.3 or pBI 121 available from Clontech in which HygeGFP replaces the beta-glucuronidase gene of the Clontech plasmids. The different Clontech plasmids vary by a reading frame shift relative to the polylinker, or the presence of the Cauliflower mosaic virus promoter.

The following examples are provided by way of illustration only, and are not intended to limit the scope of the invention disclosed herein.

EXAMPLE 1
Assay Method For Base Alteration And Preferred Oligonucleotide Selection

In this example, single-stranded and double-hairpin oligonucleotides with chimeric backbones (see Figure 1 for structures (A and B) and sequences (C and D) of assay oligonucleotides) are used to correct a point mutation in the kanamycin gene of pK^{s}m4021 (Figure 2) or the tetracycline gene of pT$^s\Delta$208 (Figure 3). All kan oligonucleotides share the same 25 base sequence surrounding the target base identified for change, just as all tet oligonucleotides do. The sequence is given in Figures 1C and Figure 1D. Each plasmid contains a functional ampicillin gene. Kanamycin gene function is restored when a G at position 4021 is converted to a C (via a substitution mutation); tetracycline gene function is restored when a deletion at position 208 is replaced by a C (via frameshift mutation). A separate plasmid, pAURNeo(-)FlAsH (Figure 9), bearing the kan^s gene is used in the cell culture experiments. This plasmid was constructed by inserting a synthetic expression cassette containing a neomycin phosphotransferase

(kanamycin resistance) gene and an extended reading frame that encodes a receptor for the FlAsH ligand into the pAUR123 shuttle vector (Panvera Corp., Madison, WI). The resulting construct replicates in *S. cerevisiae* at low copy number, confers resistance to aureobasidinA and constitutively expresses either the Neo+/FlAsH fusion product (after alteration) or the truncated Neo-/FlAsH product (before alteration) from the ADH1 promoter. By extending the reading frame of this gene to code for a unique peptide sequence capable of binding a small ligand to form a fluorescent complex, restoration of expression by correction of the stop codon can be detected in real time using confocal microscopy.

Additional constructs can be made to test additional gene alteration events or for specific use in different expression systems. For example, alternative comparable plant plasmids or integration vectors such as, e.g. those based on T-DNA, can be constructed for stable expression in plant cells according to the disclosures herein. Such constructs would use a plant specific promoter such as, e.g., cauliflower mosaic virus 35S promoter, to replace the promoters directing expression of the neo, hyg or aureobasidinA resistance gene disclosed herein, including for example, in Figures 7B, 9 and 10 herein. Moreover, the green fluorescent protein (GFP) sequence used herein may be modified to increase expression in plant cells such as Arabidopsis and the other plants disclosed herein as described in Haseloff et al., Proc. Natl.Acad. Sci. 94(6): 2122-7 (1997), Rouwendal et al. Plant Mol. Biol. 33(6): 989-99 (1997) and Hu et al. FEBS Lett. 369(2-3): 331-4 (1995). Codon usage for optimal expression of GFP in plants results from increasing the frequency of codons with a C or a G in the third position from 32 to about 60%. Specific constructs are disclosed and can be used as follows with such plant specific alterations.

We also construct three mammalian expression vectors, pHyg(rep)eGFP, pHyg(Δ)eGFP, pHyg(ins)eGFP, that contain a substitution mutation at nucleotide 137 of the hygromycin-B coding sequence. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. All point mutations create a nonsense termination codon at residue 46. We use pHYGeGFP plasmid (Invitrogen, CA) DNA as a template to introduce the mutations into the hygromycin-eGFP fusion gene by a two step site-directed mutagenesis PCR protocol. First, we generate overlapping 5' and a 3' amplicons surrounding the mutation site by PCR for each of the point mutation sites. A 215 bp 5' amplicon for the (rep), (Δ) or (ins) was generated by polymerization from oligonucleotide primer HygEGFPf (5'-AATACGACTCACTATAGG-3') to primer Hygrepr (5'GACCTATCCACGCCCTCC-3'), HygΔr (5'-GACTATCCACGCCCTCC-3'), or Hyginsr (5'-GACATTATCCACGCCCTCC-3'), respectively. We generate a 300bp 3' amplicon for the (rep), (Δ) or (ins) by polymerization from oligonucleotide primers Hygrepf (5'-CTGGGATAGGTCCTGCGG-3'), HygΔf

(5'-CGTGGATAGTCCTGCGG-3'), Hyginsf (5'-CGTGGATAATGTCCTGCGG-3'), respectively to primer HygEGFPr (5'-AAATCACGCCATGTAGTG-3'). We mix 20 ng of each of the resultant 5' and 3' overlapping amplicon mutation sets and use the mixture as a template to amplify a 523 bp fragment of the Hygromycin gene spanning the KpnI and RsrII restriction endonuclease sites. We use the Expand PCR system (Roche) to generate all amplicons with 25 cycles of denaturing at 94°C for 10 seconds, annealing at 55°C for 20 seconds and elongation at 68°C for 1 minute. We digest 10 μg of vector pHYGeGFP and 5 μg of the resulting fragments for each mutation with KpnI and RsrII (NEB) and gel purify the fragment for enzymatic ligation. We ligate each mutated insert into pHYGeGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm the mutation by Sanger dideoxy chain termination sequencing and purify the plasmid using a Qiagen maxiprep kit.

Oligonucleotide synthesis and cells. Chimeric oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) are synthesized using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, each oligonucleotide is gel-purified using, for example, procedures such as those described in Gamper *et al.*, *Biochem.* 39, 5808-5816 (2000) and the concentrations determined spectrophotometrically (33 or 40 μg/ml per A_{260} unit of single-stranded or hairpin oligomer). HUH7 cells are grown in DMEM, 10% FBS, 2mM glutamine, 0.5% pen/strep. The *E.coli* strain, DH10B, is obtained from Life Technologies (Gaithersburg, MD); DH10B cells contain a mutation in the RECA gene (*rec*A).

Cell-free extracts. Although this portion of this example is directed to mammalian systems, similar extracts from plants can be prepared as disclosed elsewhere in this application and used as disclosed in this example. We prepare cell-free extracts from HUH7 cells or other mammalian cells, as follows. We employ this protocol with essentially any mammalian cell including, for example, H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C127I (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma). We harvest approximately $2x10^8$ cells. We then wash the cells immediately in cold hypotonic buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM $MgCl_2$; 1 mM DTT) with 250 mM sucrose. We then resuspend the cells in cold hypotonic buffer without sucrose and after 15 minutes we lyse the cells with 25 strokes of a Dounce homogenizer using a tight fitting pestle. We incubate the lysed cells for 60 minutes on ice and centrifuge the sample for 15 minutes at 12000x*g*. The cytoplasmic fraction is enriched with nuclear proteins due to the extended co-incubation of the fractions following cell breakage.

We then immediately aliquote and freeze the supernatant at -80°C. We determine the protein concentration in the extract by the Bradford assay.

We also perform these experiments with cell-free extracts obtained from fungal cells, including, for example, *S. cerevisiae* (yeast), *Ustilago maydis*, and *Candida albicans*. For example, we grow yeast cells into log phase in 2L YPD medium for 3 days at 30°C. We then centrifuge the cultures at 5000x*g*, resuspend the pellets in a 10% sucrose, 50 mM Tris, 1mM EDTA lysis solution and freeze them on dry ice. After thawing, we add KCl, spermidine and lyticase to final concentrations of 0.25 mM, 5 mM and 0.1 mg/ml, respectively. We incubate the suspension on ice for 60 minutes, add PMSF and Triton X100 to final concentrations of 0.1 mM and 0.1% and continue to incubate on ice for 20 minutes. We centrifuge the lysate at 3000x*g* for 10 minutes to remove larger debris. We then remove the supernatant and clarify it by centrifuging at 30000x*g* for 15 minutes. We then add glycerol to the clarified extract to a concentration of 10% (v/v) and freeze aliquots at -80°C. We determine the protein concentration of the extract by the Bradford assay.

Reaction mixtures of 50 µl are used, consisting of 10-30 µg protein of cell-free extract, which can be optionally substituted with purified proteins or enriched fractions, about 1.5 µg chimeric double-hairpin oligonucleotide or 0.55 µg single-stranded molecule (3S/25G or 6S/25G, see Figure 1), and 1 µg of plasmid DNA (see Figures 2 and 3) in a reaction buffer of 20 mM Tris, pH 7.4, 15 mM $MgCl_2$, 0.4 mM DTT, and 1.0 mM ATP. Reactions are initiated with extract and incubated at 30°C for 45 min. The reaction is stopped by placing the tubes on ice and then immediately deproteinized by two phenol/chloroform (1:1) extractions. Samples are then ethanol precipitated. The nucleic acid is pelleted at 15,000 r.p.m. at 4°C for 30 min., is washed with 70% ethanol, resuspended in 50 µl H_20, and is stored at -20°C. 5 µl of plasmid from the resuspension (~100 ng) was transfected in 20 µl of DH10B cells by electroporation (400 V, 300 µF, 4 kΩ) in a Cell-Porator apparatus (Life Technologies). After electroporation, cells are transferred to a 14 ml Falcon snap-cap tube with 2 ml SOC and shaken at 37°C for 1 h. Enhancement of final kan colony counts is achieved by then adding 3 ml SOC with 10 µg/ml kanamycin and the cell suspension is shaken for a further 2 h at 37°C. Cells are then spun down at 3750 x g and the pellet is resuspended in 500 µl SOC. 200 µl is added undiluted to each of two kanamycin (50 µg/ml) agar plates and 200 µl of a 10^5 dilution is added to an ampicillin (100 µg/ml) plate. After overnight 37°C incubation, bacterial colonies are counted using an Accucount 1000 (Biologics). Gene conversion effectiveness is measured as the ratio of the average of the kan colonies on both plates per amp colonies multiplied by 10^{-5} to correct for the amp dilution.

The following procedure can also be used. 5 µl of resuspended reaction mixtures (total volume 50 µl) are used to transform 20 µl aliquots of electro-competent DH10B bacteria using a Cell-Porator apparatus (Life Technologies). The mixtures are allowed to recover in 1 ml SOC at 37°C for 1 hour at which time 50 µg/ml kanamycin or 12 µg/ml tetracycline is added for an additional 3 hours. Prior to plating, the bacteria are pelleted and resuspended in 200 µ1 of SOC. 100 µl aliquots are plated onto kan or tet agar plates and 100 µl of a 10^{-4} dilution of the cultures are concurrently plated on agar plates containing 100 µg/ml of ampicillin. Plating is performed in triplicate using sterile Pyrex beads. Colony counts are determined by an Accu-count 1000 plate reader (Biologics). Each plate contains 200-500 ampicillin resistant colonies or 0-500 tetracycline or kanamycin resistant colonies. Resistant colonies are selected for plasmid extraction and DNA sequencing using an ABI Prism kit on an ABI 310 capillary sequencer (PE Biosystems).

Chimeric single-stranded oligonucleotides. In Figure 1 the upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (Figure 1A) 2'-O-methyl RNA nucleotides or (Figure 1B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene.

Molecules bearing 3, 6, 8, 10 and 12 phosphorothioate linkages in the terminal regions at each end of a backbone with a total of 24 linkages (25 bases) are tested in the kan^s system. Alternatively, molecules bearing 2, 4, 5, 7, 9 and 11 in the terminal regions at each end are tested. The results of one such experiment, presented in Table 1 and Figure 1B, illustrate an enhancement of correction activity directed by some of these modified structures. In this illustrative example, the most efficient molecules contained 3 or 6 phosphorothioate linkages at each end of the 25-mer; the activities are approximately equal (molecules IX and X with results of 3.09 and 3.7 respectively). A reduction in alteration activity may be observed as the number of modified linkages in the molecule is further increased. Interestingly, a single-strand molecule containing 24 phosphorothioate linkages is minimally active suggesting that this backbone modification when used throughout the molecule supports only a low level of targeted gene repair or alteration. Such a non-altering, completely modified molecule can provide a baseline control for determining efficiency of correction for a specific oligonucleotide molecule of known sequence in defining the optimum oligonucleotide for a particular alteration event.

The efficiency of gene repair directed by phosphorothioate-modified, single-stranded molecules, in a length dependent fashion, led us to examine the length of the RNA modification used in

the original chimera as it relates to correction. Construct III represents the "RNA-containing" strand of chimera I and, as shown in Table 1 and Figure 2A, it promotes inefficient gene repair. But, as shown in the same figure, reducing the RNA residues on each end from 10 to 3 increases the frequency of repair. At equal levels of modification, however, 25-mers with 2'-O-methyl ribonucleotides were less effective gene repair agents than the same oligomers with phosphorothioate linkages. These results reinforce the fact that an RNA containing oligonucleotide is not as effective in promoting gene repair or alteration as a modified DNA oligonucleotide.

Repair of the kanamycin mutation requires a G→C exchange. To confirm that the specific desired correction alteration was obtained, colonies selected at random from multiple experiments are processed and the isolated plasmid DNA is sequenced. As seen in Figure 4, colonies generated through the action of the single-stranded molecules 3S/25G (IX), 6S/25G (X) and 8S/25G (XI) respectively contained plasmid molecules harboring the targeted base correction. While a few colonies appeared on plates derived from reaction mixtures containing 25-mers with 10 or 12 thioate linkages on both ends, the sequences of the plasmid molecules from these colonies contain nonspecific base changes. In these illustrative examples, the second base of the codon is changed (see Figure 3). These results show that modified single-strands can direct gene repair, but that efficiency and specificity are reduced when the 25-mers contain 10 or more phosphorothioate linkages at each end.

In Figure 1, the numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the examplified molecule although other molecules with 2, 4, 5, 7, 9 and 11 modifications at each end can also be tested. Hence oligo 12S/25G represents a 25-mer oligonucleotide which contains 12 phosphorothioate linkages on each side of the central G target mismatch base producing a fully phosphorothioate linked backbone, displayed as a dotted line. The dots are merely representative of a linkage in the figure and do not depict the actual number of linkages of the oligonucleotide. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G).

Correction of a mutant kanamycin gene in cultured mammalian cells. Although this portion of this example is directed to cultured mammalian cells, comparable methods may be used using cultured plant cells or protoplasts of those cells from the plant species disclosed herein. The experiments are performed using different eukaryotic cells including plant and mammalian cells, including, for example, 293 cells (transformed human primary kidney cells), HeLa cells (human cervical carcinoma), and H1299 (human epithelial carcinoma, non-small cell lung cancer). HeLa cells are grown at 37°C and 5% CO_2 in a humidified incubator to a density of 2 x 10^5 cells/ml in an 8 chamber slide (Lab-Tek). After replacing the

regular DMEM with Optimem, the cells are co-transfected with 10 μg of plasmid pAURNeo(-)FlAsH and 5 μg of modified single-stranded oligonucleotide (3S/25G) that is previously complexed with 10 μg lipofectamine, according to the manufacturer's directions (Life Technologies). The cells are treated with the liposome-DNA-oligo mix for 6 hrs at 37°C. Treated cells are washed with PBS and fresh DMEM is added. After a 16-18 hr recovery period, the culture is assayed for gene repair. The same oligonucleotide used in the cell-free extract experiments is used to target transfected plasmid bearing the kan^s gene. Correction of the point mutation in this gene eliminates a stop codon and restores full expression. This expression can be detected by adding a small non-fluorescent ligand that bound to a C-C-R-E-C-C sequence in the genetically modified carboxy terminus of the kan protein, to produce a highly fluorescent complex (FlAsH system, Aurora Biosciences Corporation). Following a 60 min incubation at room temperature with the ligand (FlAsH-EDT2), cells expressing full length kan product acquire an intense green fluorescence detectable by fluorescence microscopy using a fluorescein filter set. Similar experiments are performed using the HygeGFP target as described in Example 2 with a variety of mammalian cells, including, for example, COS-1 and COS-7 cells (African green monkey), and CHO-K1 cells (Chinese hamster ovary). The experiments are also performed with PG12 cells (rat pheochromocytoma) and ES cells (human embryonic stem cells).

Summary of experimental results. Tables 1, 2 and 3 respectively provide data on the efficiency of gene repair directed by single-stranded oligonucleotides. Table 1 presents data using a cell-free extract from human liver cells (HUH7) to catalyze repair of the point mutation in plasmid pkan^{s}m4021 (see Figure 1). Table 2 illustrates that the oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity. Table 3 illustrates data from the repair of a frameshift mutation (Figure 3) in the tet gene contained in plasmid pTetΔ208. Table 4 illustrates data from repair of the pkan^{s}m4021 point mutation catalyzed by plant cell extracts prepared from canola and musa (banana). Colony numbers are presented as kan^r or tet^r and fold increases (single strand versus double hairpin) are presented for kan^r in Table 1.

Figure 5A is a confocal picture of HeLa cells expressing the corrected fusion protein from an episomal target. Gene repair is accomplished by the action of a modified single-stranded oligonucleotide containing 3 phosphorothioate linkages at each end (3S/25G). Figure 5B represents a "Z-series" of HeLa cells bearing the corrected fusion gene. This series sections the cells from bottom to top and illustrates that the fluorescent signal is "inside the cells".

Results. In summary, we have designed a novel class of single-stranded oligonucleotides with backbone modifications at the termini and demonstrate gene repair/conversion

activity in mammalian and plant cell-free extracts. We confirm that the all DNA strand of the RNA-DNA double-stranded double hairpin chimera is the active component in the process of gene repair. In some cases, the relative frequency of repair by the novel oligonucleotides of the invention is elevated approximately 3-4-fold in certain embodiments when compared to frequencies directed by chimeric RNA-DNA double hairpin oligonucleotides.

This strategy centers around the use of extracts from various sources to correct a mutation in a plasmid using a modified single-stranded or a chimeric RNA-DNA double hairpin oligonucleotide. A mutation is placed inside the coding region of a gene conferring antibiotic resistance in bacteria, here kanamycin or tetracycline. The appearance of resistance is measured by genetic readout in *E.coli* grown in the presence of the specified antibiotic. The importance of this system is that both phenotypic alteration and genetic inheritance can be measured. Plasmid pK^{s}m4021 contains a mutation (T➜G) at residue 4021 rendering it unable to confer antibiotic resistance in *E.coli*. This point mutation is targeted for repair by oligonucleotides designed to restore kanamycin resistance. To avoid concerns of plasmid contamination skewing the colony counts, the directed correction is from G➜C rather than G➜T (wild-type). After isolation, the plasmid is electroporated into the DH10B strain of *E.coli*, which contains inactive RecA protein. The number of kanamycin colonies is counted and normalized by ascertaining the number of ampicillin colonies, a process that controls for the influence of electroporation. The number of colonies generated from three to five independent reactions was averaged and is presented for each experiment. A fold increase number is recorded to aid in comparison.

The original RNA-DNA double hairpin chimera design, e.g., as disclosed in U.S. Patent 5,565,350, consists of two hybridized regions of a single-stranded oligonucleotide folded into a double hairpin configuration. The double-stranded targeting region is made up of a 5 base pair DNA/DNA segment bracketed by 10 base pair RNA/DNA segments. The central base pair is mismatched to the corresponding base pair in the target gene. When a molecule of this design is used to correct the kan^s mutation, gene repair is observed (I in Figure 1A). Chimera II (Figure 1B) differs partly from chimera I in that only the DNA strand of the double hairpin is mismatched to the target sequence. When this chimera was used to correct the kan^s mutation, it was twice as active. In the same study, repair function could be further increased by making the targeting region of the chimera a continuous RNA/DNA hybrid.

Frame shift mutations are repaired. By using plasmid pT$^s\Delta$208, described in Figure 1(C) and Figure 3, the capacity of the modified single-stranded molecules that showed activity in correcting a point mutation, can be tested for repair of a frameshift. To determine efficiency of correction of the mutation, a chimeric oligonucleotide (Tet I), which is designed to insert a T residue at position 208, is

used. A modified single-stranded oligonucleotide (Tet IX) directs the insertion of a T residue at this same site. Figure 3 illustrates the plasmid and target bases designated for change in the experiments. When all reaction components are present (extract, plasmid, oligomer), tetracycline resistant colonies appear. The colony count increases with the amount of oligonucleotide used up to a point beyond which the count falls off (Table 3). No colonies above background are observed in the absence of either extract or oligonucleotide, nor when a modified single-stranded molecule bearing perfect complementarity is used. Figure 3 represents the sequence surrounding the target site and shows that a T residue is inserted at the correct site. We have isolated plasmids from fifteen colonies obtained in three independent experiments and each analyzed sequence revealed the same precise nucleotide insertion. These data suggest that the single-stranded molecules used initially for point mutation correction can also repair nucleotide deletions.

Comparison of phosphorothioate oligonucleotides to 2'-O-methyl substituted oligonucleotides. From a comparison of molecules VII and XI, it is apparent that gene repair is more subject to inhibition by RNA residues than by phosphorothioate linkages. Thus, even though both of these oligonucleotides contain an equal number of modifications to impart nuclease resistance, XI (with 16 phosphorothioate linkages) has good gene repair activity while VII (with 16 2'-O-methyl RNA residues) is inactive. Hence, the original chimeric double hairpin oligonucleotide enabled correction directed, in large part, by the strand containing a large region of contiguous DNA residues.

Oligonucleotides can target multiple nucleotide alterations within the same template. The ability of individual single-stranded oligonucleotides to correct multiple mutations in a single target template is tested using the plasmid pK^{s}m4021 and the following single-stranded oligonucleotides modified with 3 phosphorothioate linkages at each end (indicated as underlined nucleotides): Oligo1 is a 25-mer with the sequence <u>TTC</u>GATAAGCCTA**T**G**C**TGACCC<u>GTG</u> corrects the original mutation present in the kanamycin resistance gene of pK^{s}m4021 as well as directing another alteration 2 basepairs away in the target sequence (both indicated in boldface); Oligo2 is a 70-mer with the 5'-end sequence <u>TTC</u>GGCTACGACTGGGCACAACAGACAATTGGC with the remaining nucleotides being completely complementary to the kanamycin resistance gene and also ending in 3 phosphorothioate linkages at the 3' end. Oligo2 directs correction of the mutation in pK^{s}m4021 as well as directing another alteration 21 basepairs away in the target sequence (both indicated in boldface).

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pK^{s}M4021 plasmid. These include, for example, a second 25-mer that alters two nucleotides that are three nucleotides apart with the sequence 5'-

TTGTGCCCAGTC**<u>G</u>**TA**<u>T</u>**CCGAATAGC-3'; a 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-CATCAGAGCAGCC**<u>A</u>**ATTGTCTGTTGTGCCCAGTC**<u>G</u>**TAGCCGAA TAGCCTCTCCACCCAAGCGGCCGGAGA-3'; and another 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-GCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC**<u>A</u>**ATTGTCTGTTGTGCCCAGTC**<u>G</u>**TAGCCGAAT AGCCT-3'. The nucleotides in the oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same way as the other oligonucleotides of the invention.

We assay correction of the original mutation in pK^{s}m4021 by monitoring kanamycin resistance (the second alterations which are directed by Oligo2 and Oligo3 are silent with respect to the kanamycin resistance phenotype). In addition, in experiments with Oligo2, we also monitor cleavage of the resulting plasmids using the restriction enzyme Tsp509I which cuts at a specific site present only when the second alteration has occurred (at ATT in Oligo2). We then sequence these clones to determine whether the additional, silent alteration has also been introduced. The results of an analysis are presented below:

	Oligo1 (25-mer)	Oligo2 (70-mer)
Clones with both sites changed	9	7
Clones with a single site changed	0	2
Clones that were not changed	4	1

Nuclease sensitivity of unmodified DNA oligonucleotide. Electrophoretic analysis of nucleic acid recovered from the cell-free extract reactions conducted here confirm that the unmodified single-stranded 25-mer did not survive incubation whereas greater than 90% of the terminally modified oligos did survive (as judged by photo-image analyses of agarose gels).

Plant extracts direct repair. The modified single-stranded constructs can be tested in plant cell extracts. We have observed gene alteration using extracts from multiple plant sources, including, for example, Arabidopsis, tobacco, banana, maize, soybean, canola, wheat, spinach as well as spinach chloroplast extract or extracts made from other plant cells disclosed herein. We prepare the extracts by grinding plant tissue or cultured cells under liquid nitrogen with a mortar and pestle. We extract 3 ml of the ground plant tissue with 1.5 ml of extraction buffer (20 mM HEPES, pH7.5; 5 mM KCl;

1.5 mM $MgCl_2$; 10 mM DTT; and 10% [v/v] glycerol). Some plant cell-free extracts also include about 1% (w/v) PVP. We then homogenize the samples with 15 strokes of a Dounce homogenizer. Following homogenization, we incubate the samples on ice for 1 hour and centrifuge at 3000 x *g* for 5 minutes to remove plant cell debris. We then determine the protein concentration in the supernatants (extracts) by Bradford assay. We dispense 100 µg (protein) aliquots of the extracts which we freeze in a dry ice-ethanol bath and store at -80°C.

We describe experiments using two sources here: a dicot (canola) and a monocot (banana, *Musa acuminata* cv. Rasthali). Each vector directs gene repair of the kanamycin mutation (Table 4); however, the level of correction is elevated 2-3 fold relative to the frequency observed with the chimeric oligonucleotide. These results are similar to those observed in the mammalian system wherein a significant improvement in gene repair occurred when modified single-stranded molecules were used.

Tables are attached hereto.

Table I

Gene repair activity is directed by single-stranded oligonucleotides.

Oligonucleotide	Plasmid	Extract (ug)	kan^r colonies	Fold increase
I	pK^{S}m4021	10	300	
I		20	418	1.0x
II		10	537	
II		20	748	1.78x
III		10	3	
III		20	5	0.01x
IV		10	112	
IV		20	96	0.22x
V		10	217	
V		20	342	0.81x
VI		10	6	
VI		20	39	0.093x
VII		10	0	
VII		20	0	0x
VIII		10	3	
VIII		20	5	0.01x
IX		10	936	
IX		20	1295	3.09x
X		10	1140	
X		20	1588	3.7x
XI		10	480	
XI		20	681	1.6x
XII		10	18	
XII		20	25	0.059x
XIII		10	0	
XIII		20	4	0.009x
-		20	0	
I		-	0	

Plasmid pK^{s}m4021 (1 μg), the indicated oligonucleotide (1.5 μg chimeric oligonucleotide or 0.55 μg single-stranded oligonucleotide; molar ratio of oligo to plasmid of 360 to 1) and either 10 or 20 μg of HUH7 cell-free extract were incubated 45 min at 37°C. Isolated plasmid DNA was electroporated into *E. coli* (strain DH10B) and the number of kan^r colonies counted. The data represent the number of kanamycin resistant colonies per 10^6 ampicillin resistant colonies generated from the same reaction and is the average of three

experiments (standard deviation usually less than +/- 15%). Fold increase is defined relative to 418 kan^r colonies (second reaction) and in all reactions was calculated using the 20μg sample.

Table II

Modified single-stranded oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity.

A.

Oligonucleotide	Plasmid	Extract	kan^r colonies
IX (3S/25G)	↓	HUH7	637
X (6S/25G)		HUH7	836
IX		$MEF2^{-/-}$	781
X		$MEF2^{-/-}$	676
IX		$MEF3^{-/-}$	582
X		$MEF3^{-/-}$	530
IX		$MEF^{+/+}$	332
X		$MEF^{+/+}$	497
-		$MEF2^{-/-}$	10
-		$MEF3^{-/-}$	5
-		$MEF^{+/+}$	14

Chimeric oligonucleotide (1.5 μg) or modified single-stranded oligonucleotide (0.55 μg) was incubated with 1μg of plasmid pK^sm4021 and 20μg of the indicated extracts. MEF represents mouse embryonic fibroblasts with either MSH2 ($2^{-/-}$) or MSH3 ($3^{-/-}$) deleted. $MEF^{+/+}$ indicates wild-type mouse embryonic fibroblasts. The other reaction components were then added and processed through the bacterial readout system. The data represent the number of kanamycin resistant colonies per 10^6 ampicillin resistant colonies.

Table III

Frameshift mutation repair is directed by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	tet^r colonies
Tet IX (3S/25A; 0.5 μg)	$pT^s\Delta208$ (1μg)	-	0
-	↓	20μg	0
Tet IX (0.5 μg)	↓	↓	48
Tet IX (1.5 μg)	↓	↓	130
Tet IX (2.0 μg)	↓	↓	68
Tet I (chimera; 1.5 μg)	↓	↓	48

Each reaction mixture contained the indicated amounts of plasmid and oligonucleotide. The extract used for these experiments came from HUH7 cells. The data represent the number of tetracycline resistant colonies per 10^6 ampicillin resistant colonies generated from the same reaction and is the average of 3 independent experiments. Tet I is a chimeric oligonucleotide and Tet IX is a modified single-stranded oligonucleotide that are designed to insert a T residue at position 208 of $pT^s\Delta208$. These oligonucleotides are equivalent to structures I and IX in Figure 2.

Table IV

Plant cell-free extracts support gene repair by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	kan^r colonies
II (chimera)	pK^{S}m4021	30μg Canola	337
IX (3S/25G)	↓	Canola	763
X (6S/25G)	↓	Canola	882
II	↓	*Musa*	203
IX	↓	*Musa*	343
X	↓	*Musa*	746
-	↓	Canola	0
-	↓	*Musa*	0
IX	↓	- Canola	0
X	↓	- *Musa*	0

Canola or Musa cell-free extracts were tested for gene repair activity on the kanamycin-sensitive gene as previously described in (18). Chimeric oligonucleotide II (1.5 μg) and modified single-stranded oligonucleotides IX and X (0.55μg) were used to correct pK^{S}m4021. Total number of kan^r colonies are present per 10^7 ampicillin resistant colonies and represent an average of four independent experiments.

Table V

Gene repair activity in cell-free extracts prepared from yeast (Saccharomyces cerevisiae)

Cell-type	Plasmid	Chimeric Oligo	SS Oligo	$kan^r/amp^r \times 10^6$
Wild type	pKan^{s}m4021	1μg		0.36
Wild type			1μg	0.81
ΔRAD52		1μg		10.72
ΔRAD52			1μg	17.41
ΔPMS1		1μg		2.02
ΔPMS1			1μg	3.23

In this experiment, the kan^s gene in pKan^{s}4021 is corrected by either a chimeric double-hairpin oligonucleotide or a single-stranded oligonucleotide containing three thioate linkages at each end (3S/25G).

EXAMPLE 2
Yeast Cell Targeting Assay Method for Base Alteration and Preferred Oligonucleotide Selection

In this example, single-stranded oligonucleotides with modified backbones and double-hairpin oligonucleotides with chimeric, RNA-DNA backbones are used to measure gene repair using two episomal targets with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair. These plasmids are pAURHYG(rep)GFP, which contains a point mutation in the hygromycin resistance gene (Figure 7), pAURHYG(ins)GFP, which contains a single-base insertion in the hygromycin resistance gene (Figure 7) and pAURHYG(Δ)GFP which has a single base deletion. We also use the plasmid containing a wild-type copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)GFP, as a control. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, at codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In pAURHYG(ins)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, at codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene.

We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)EGFP and ligation into pAUR123 (Panvera, CA). We digest 10 μg pAUR123 vector DNA, as well as, 10 μg of each pHyg(x)EGFP construct with KpnI and SalI (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify using a Qiagen maxiprep kit.

We use this system to assay the ability of five oligonucleotides (shown in Figure 8) to support correction under a variety of conditions. The oligonucleotides which direct correction of the mutation in pAURHYG(rep)GFP can also direct correction of the mutation in pAURHYG(ins)GFP. Three of the four oligonucleotides (HygE3T/25, HygE3T/74 and HygGG/Rev) share the same 25-base sequence surrounding the base targeted for alteration. HygGG/Rev is an RNA-DNA chimeric double hairpin

oligonucleotide of the type described in the prior art. One of these oligonucleotides, HygE3T/74, is a 74-base oligonucleotide with the 25-base sequence centrally positioned. The fourth oligonucleotide, designated HygE3T/74α, is the reverse complement of HygE3T/74. The fifth oligonucleotide, designated Kan70T, is a non-specific, control oligonucleotide which is not complementary to the target sequence. Alternatively, an oligonucleotide of identical sequence but lacking a mismatch to the target or a completely thioate modified oligonucleotide or a completely 2-0-methylated modified oligonucleotide may be used as a control. Alternatively, oligonucleotides containing one, two, three, four, five, six, eight, ten or more LNA modifications on at least one of the two termini (and preferrably the 3' terminus) may be used in different embodiments.

Oligonucleotide synthesis and cells. We synthesized and purified the chimeric, double-hairpin oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) as described in Example 1. Plasmids used for assay were maintained stably in yeast (*Saccharomyces cerevisiae*) strain LSY678 *MATα* at low copy number under aureobasidin selection. Plasmids and oligonucleotides are introduced into yeast cells by electroporation as follows: to prepare electrocompetent yeast cells, we inoculate 10 ml of YPD media from a single colony and grow the cultures overnight with shaking at 300 rpm at 30°C. We then add 30 ml of fresh YPD media to the overnight cultures and continue shaking at 30°C until the OD_{600} was between 0.5 and 1.0 (3-5 hours). We then wash the cells by centrifuging at 4°C at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We then centrifuge at 4°C at 3000 rpm for 5 minutes and resuspend in 1 ml ice-cold 1M sorbitol and then finally centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the cells in 120 μl 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40 μl of cells with 5 μg of nucleic acid, unless otherwise stated, and incubate on ice for 5 minutes. We then transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene Pulser apparatus at 1.5 kV, 25 μF, 200 Ω for one five-second pulse. We then immediately resuspend the cells in 1 ml YPD supplemented with 1M sorbitol and incubate the cultures at 30°C with shaking at 300 rpm for 6 hours. We then spread 200 μl of this culture on selective plates containing 300 μg/ml hygromycin and spread 200 μl of a 10^5 dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We then count the colonies on the plates and calculate the gene conversion efficiency by determining the number of hygromycin resistance colonies per 10^5 aureobasidinA resistant colonies.

Frameshift mutations are repaired in yeast cells. We test the ability of the oligonucleotides shown in Figure 8 to correct a frameshift mutation *in vivo* using LSY678 yeast cells

containing the plasmid pAURHYG(ins)GFP. These experiments, presented in Table 6, indicate that these oligonucleotides can support gene correction in yeast cells. These data reinforce the results described in Example 1 indicating that oligonucleotides comprising phosphorothioate linkages facilitate gene correction much more efficiently than control duplex, chimeric RNA-DNA oligonucleotides. This gene correction activity is also specific as transformation of cells with the control oligonucleotide Kan70T produced no hygromycin resistant colonies above background and thus Kan70T did not support gene correction in this system. In addition, we observe that the 74-base oligonucleotide (HygE3T/74) corrects the mutation in pAURHYG(ins)GFP approximately five-fold more efficiently than the 25-base oligonucleotide (HygE3T/25). We also perform control experiments with LSY678 yeast cells containing the plasmid pAURHYG(wt)GFP. With this strain we observed that even without added oligonucleotides, there are too many hygromycin resistant colonies to count.

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pAURHYG(x)eGFP plasmid. These include, for example, one that alters two basepairs that are 3 nucleotides apart is a 74-mer with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGG<u>**G**</u>TA<u>**C**</u>GTCCTGCGGGTAAATAGCTGCGCCGATG GTTTCTAC-3'; a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATA<u>**C**</u>GTCCTGCGGGTAAA<u>**C**</u>AGCTGCGCCGATG GTTTCTAC-3'; and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATA<u>**C**</u>GTCCTGCGGGTAAATAGCTGCGCCGA<u>**C**</u>G GTTTCTAC. The nucleotides in these oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same ways as the other oligonucleotides of the invention.

Oligonucleotides targeting the sense strand direct gene correction more efficiently. We compare the ability of single-stranded oligonucleotides to target each of the two strands of the target sequence of both pAURHYG(ins)GFP and pAURHYG(rep)GFP. These experiments, presented in Tables 7 and 8, indicate that an oligonucleotide, HygE3T/74α, with sequence complementary to the sense strand (i.e. the strand of the target sequence that is identical to the mRNA) of the target sequence facilitates gene correction approximately ten-fold more efficiently than an oligonucleotide, HygE3T/74, with sequence complementary to the non-transcribed strand which serves as the template for the synthesis of RNA. As indicated in Table 7, this effect was observed over a range of oligonucleotide concentrations from 0-3.6 μg, although we did observe some variability in the difference between the two oligonucleotides (indicated in Table 7 as a fold difference between HygE3T/74α and HygE3T/74).

Furthermore, as shown in Table 8, we observe increased efficiency of correction by HygE3T/74α relative to HygE3T/74 regardless of whether the oligonucleotides were used to correct the base substitution mutation in pAURHYG(rep)GFP or the insertion mutation in pAURHYG(ins)GFP. The data presented in Table 8 further indicate that the single-stranded oligonucleotides correct a base substitution mutation more efficiently than an insertion mutation. However, this last effect was much less pronounced and the oligonucleotides of the invention are clearly able efficiently to correct both types of mutations in yeast cells. In addition, the role of transcription is investigated using plasmids with inducible promoters such as that described in Figure 10.

Optimization of oligonucleotide concentration. To determine the optimal concentration of oligonucleotide for the purpose of gene alteration, we test the ability of increasing concentrations of Hyg3T/74α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678. We chose this assay system because our previous experiments indicated that it supports the highest level of correction. However, this same approach could be used to determine the optimal concentration of any given oligonucleotide. We test the ability of Hyg3T/74α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678 over a range of oligonucleotide concentrations from 0-10.0 μg. As shown in Table 9, we observe that the correction efficiency initially increases with increasing oligonucleotide concentration, but then declines at the highest concentration tested.

Tables are attached hereto.

Table 6

Correction of an insertion mutation in pAURHYG(ins)GFP by HygGG/Rev, HygE3T/25 and HygE3T/74

Oligonucleotide Tested	Colonies on Hygromycin	Colonies on Aureobasidin (/10^5)	Correction Efficiency
HygGG/Rev	3	157	0.02
HygE3T/25	64	147	0.44
HygE3T/74	280	174	1.61
Kan70T	0	—	—

Table 7

An oligonucleotide targeting the sense strand of the target sequence corrects more efficiently.

Amount of Oligonucleotide (μg)	Colonies per hygromycin plate	
	HygE3T/74	HygE3T/74α
0	0	0
0.6	24	128 (8.4x)*
1.2	69	140 (7.5x)*
2.4	62	167 (3.8x)*
3.6	29	367 (15x)*

* The numbers in parentheses represent the fold increase in efficiency for targeting the non-transcribed strand as compared to the other strand of a DNA duplex that encodes a protein.

Table 8

Correction of a base substitution mutation is more efficient than correction of a frame shift mutation.

Oligonucleotide Tested (5 μg)	Plasmid tested (contained in LSY678)	
	pAURHYG(ins)GFP	pAURHYG(rep)GFP
HygE3T/74	72	277
HygE3T/74α	1464	2248
Kan70T	0	0

Table 9

Optimization of oligonucleotide concentration in electroporated yeast cells.

Amount (μg)	Colonies on hygromycin	Colonies on aureobasidin ($/10^5$)	Correction efficiency
0	0	67	0
1.0	5	64	0.08
2.5	47	30	1.57
5.0	199	33	6.08
7.5	383	39	9.79
10.0	191	33	5.79

Example 3
Cultured Cell Manipulation

Although disclosure in this example is directed to use of stem cells or human blood cells and microinjection, the microinjection procedures may also be used with cultured plant cells or protoplasts using any plant species, including those disclosed herein. Mononuclear cells are isolated from human umbilical cord blood of normal donors using Ficoll Hypaque (Pharmacia Biotech, Uppsala, Sweden) density centrifugation. CD34+ cells are immunomagnetically purified from mononuclear cells using either

the progenitor or Multisort Kits (Miltenyi Biotec, Auburn, CA). $Lin^{-}CD38^{-}$ cells are purified from the mononuclear cells using negative selection with StemSep system according to the manufacturer's protocol (Stem Cell Technologies, Vancouver, CA). Cells used for microinjection are either freshly isolated or cryopreserved and cultured in Stem Medium (S Medium) for 2 to 5 days prior to microinjection. S Medium contains Iscoves' Modified Dulbecco's Medium without phenol red (IMDM) with 100 μg/ml glutamine/penicillin/streptomycin, 50 mg/ml bovine serum albumin, 50 μg/ml bovine pancreatic insulin, 1 mg/ml human transferrin, and IMDM; Stem Cell Technologies), 40 μg/ml low-density lipoprotein (LDL; Sigma, St. Louis, MO), 50 mM HEPEs buffer and 50 μM 2-mercaptoethanol, 20 ng/ml each of thrombopoietin, flt-3 ligand, stem cell factor and human IL-6 (Pepro Tech Inc., Rocky Hill, NJ). After microinjection, cells are detached and transferred in bulk into wells of 48 well plates for culturing.

35 mm dishes are coated overnight at 4° C with 50 μg/ml Fibronectin (FN) fragment CH-296 (Retronectin; TaKaRa Biomedicals, Panvera, Madison, WI) in phosphate buffered saline and washed with IMDM containing glutamine/penicillin/streptomycin. 300 to 2000 cells are added to cloning rings and attached to the plates for 45 minutes at 37° C prior to microinjection. After incubation, cloning rings are removed and 2 ml of S Medium are added to each dish for microinjection. Pulled injection needles with a range of 0.22 μm to 0.3 μm outer tip diameter are used. Cells are visualized with a microscope equipped with a temperature controlled stage set at 37° C and injected using an electronically interfaced Eppendorf Micromanipulator and Transjector. Successfully injected cells are intact, alive and remain attached to the plate post injection. Molecules that are flourescently labeled allow determination of the amount of oligonucleotide delivered to the cells.

For *in vitro* erythropoiesis from $Lin^{-}CD38^{-}$ cells, the procedure of Malik, 1998 can be used. Cells are cultured in ME Medium for 4 days and then cultured in E Medium for 3 weeks. Erythropoiesis is evident by glycophorin A expression as well as the presence of red color representing the presence of hemoglobin in the cultured cells. The injected cells are able to retain their proliferative capacity and the ability to generate myeloid and erythoid progeny. CD34+ cells can convert a normal A (β^A) to sickle T (β^S) mutation in the β-globin gene or can be altered using any of the oligonucleotides of the invention herein for correction or alteration of a normal gene to a mutant gene. Alternatively, stem cells can be isolated from blood of humans having genetic disease mutations and the oligonucleotides of the invention can be used to correct a defect or to modify genomes within those cells.

Alternatively, non-stem cell populations of cultured cells can be manipulated using any method known to those of skill in the art including, for example, the use of polycations, cationic lipids,

liposomes, polyethylenimine (PEI), electroporation, biolistics, calcium phosphate precipitation, or any other method known in the art.

Biolistic delivery of oligonucleotide into plant cells may be accomplished according to the following method. One milliliter of packed cell volume of plant cell suspensions are subcultured onto plates containing solid medium [with Murashige and Skoog salts from Gibco/BRL, 500 mg/liter Mes, 1 mg/liter thiamin, 100 mg/liter myo-inositol, 180 mg/liter KH2PO4, 2.21 mg/liter 2,4-dichlorophenoxyacetic acid (2,4-D), and 30 g/liter sucrose (pH 5.7) and having 8 g/liter agar-agar from Sigma added before autoclaving]. By using a helium-driven particle gun such as that from BioRad and following manufacturers directions, oligonucleotides may be introduced to cells after precipitation onto 1 micrometer or comparable gold microcarriers (Bio-Rad). To precipitate onto microcarriers, 35 microliters of a particle suspension (60 mg of microcarriers per ml of 100% ethanol) is transferred to a 1.5 ml microcentrifuge tube, which is agitated on a vortex mixer. Then 40 microliter of resuspended oligonucleotide (60 ng/microliter water) is added; then 75 microliter of ice-cold 2.5 M CaCl2 is added; then 75 microliter of ice-cold 0.1 M spermidine is added. The tube is mixed vigorously or a vortex mixer for 10 min at room temperature. The particles are allowed to settle for 10 min and are centrifuged at 11,750 g for 30 sec. The supernatant is removed and the particles are resuspended in 50 microliter of 100% ethanol. An aliquot of 10 microliter of the resuspended particles are applied to each macro-projectile which is used to bombard each plate once at 900 psi (1 psi = 6.89 kPa) with a gap distance (distance from power source to macroprojectile) of 1 cm and a target distance (distance from microprojectile launch site to target material) of 10 cm.

An alternative method of delivery can be used as follows. Cultured cells are suspended in liquid N6 medium and then plated on a VWR Scientific glass fiber filter. About 0.4 microgram of oligonucleotide are precipitated with 15 microliter of 2.5 mM CaCl2 and 5 microliter of 0.1 M spermidine onto 25 microgram of 1.0 micrometer gold particles. Microprojectile bombardment is performed by using a Bio-Rad PDS-1000 He particle delivery system or comparable machine following manufacturers instructions. Alterations in oligonucleotide concentrations can be employed to determine the optimum concentration of oligonucleotide according to the procedures described herein for any particular oligonucleotide of the invention.

Alternatively, the oligonucleotide of the invention may be delivered to a plant cell by electroporation of a protoplast derived from a plant part. The protoplasts may be formed by enzymatic treatment of a plant part, particularly a leaf, according to techniques such as those in Gallois et al., Methods in Molecular Biology 55: 89-107 by Humana Press. Such conditions for electroporation use

about 3 x 10^5 protoplasts in a total volume of about 0.3 ml with a concentration of oligonucleotide of between 0.6 to 4 microgram per ml.

EXAMPLE 4

Plant Cells

The oligonucleotides of the invention can also be used to repair or direct a mutagenic event in plants and animal cells. Although little information is available on plant mutations amongst natural cultivars, the oligonucleotides of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying Gln can be modified at a specific site to TAA; a AAG codon specifying Lys can be modified to UAG at a specific site; and a CGA codon for Arg can be modified to a UGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a defective truncated protein, shortened at the site of the stop codon

. Alternatively, frameshift additions or deletions can be directed into the genome at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

For introduction of a T-DNA, including the T-DNA in the plasmid of Figure 11, into a plant cell, *Agrobacterium tumefaciens* is used. These techniques are routine standard techniques known in the art. For example, one method follows. We transform *A. tumefaciens* is transformed by electroporation (using a BioRad Gene Pulser™). Competent *A. tumefaciens* is prepared using a method similar to that of preparing competent *E. coli* by suspending a freshly grown culture three times in ice-cold water and a final resuspension in 10% glycerol. Electroporation conditions are a 0.2 cm gap cuvette at a setting of 25 μF, 200 Ω and 2.5 kV.

A. tumefaciens containing a plasmid with a T-DNA is then used to introduce the T-DNA into a plant cell using routine standard techniques known in the art. For example, we transform Arabidopsis by vacuum infiltration or by dipping flowers in an Agrobacterium solution containing a surfactant, e.g. L-77. Seeds are then collected, grown and screened for presence of the T-DNA. Alternatively, Agrobacterium can be used to transform callus tissue and the callus tissue can then be used to regenerate transformed plants.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some

detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Notes on the tables presented below:

Each of the following tables presents, for the specified gene, a plurality of mutations that are known to confer a relevant phenotype and, for each mutation, the oligonucleotides that can be used to correct the respective mutation site-specifically in the genome according to the present invention.

The left-most column identifies each alteration or mutation and the phenotype that the alteration/mutation confers.

For most entries, the mutation/alteration is identified at both the nucleic acid and protein level. At the amino acid level, mutations are presented according to the following standard nomenclature. The centered number identifies the position of the mutated codon in the protein sequence; to the left of the number is the wild type residue and to the right of the number is the mutant codon. Terminator codons are shown as "TERM". At the nucleic acid level, the entire triplet of the wild type and mutated codons is shown.

The middle column presents, for each mutation, four oligonucleotides capable of repairing the mutation site-specifically in the genome or in cloned DNA including DNA in artificial chromosomes, episomes, plasmids, or other types of vectors. The oligonucleotides of the invention, however, may include any of the oligonucleotides sharing portions of the sequence of the 121 base sequence. Thus, oligonucleotides of the invention for each of the depicted targets may be 18, 19, 20 up to about 121 nucleotides in length. Sequence may be added non-symmetrically.

All oligonucleotides are presented, per convention, in the 5' to 3' orientation. The nucleotide that effects the change in the genome is underlined and presented in bold.

The first of the four oligonucleotides for each mutation is a 121 nt oligonucleotide centered about the repair/altering nucleotide. The second oligonucleotide, its reverse complement, targets the opposite strand of the DNA duplex for repair/alteration. The third oligonucleotide is the minimal 17 nt domain of the first oligonucleotide, also centered about the repair/alteration nucleotide. The fourth oligonucleotide is the reverse complement of the third, and thus represents the minimal 17 nt domain of the second.

The third column of each table presents the SEQ ID NO: of the respective repair oligonucleotide.

Example 5

Engineering herbicide resistant plants

Chemical weed control is an important tool of modern agriculture and many herbicides have been developed for this purpose. Their use has resulted in substantial increases in the yields of many crops, including, for example, maize, soybeans, and cotton. Thus while the use of fertilizers and new high-yielding crop varieties have contributed greatly to the "green revolution," chemical weed control has also been at the forefront of technological achievement.

Herbicides having broad-spectrum activity are particularly useful because they obviate the need for multiple herbicides targeting different classes of weeds. The problem with such herbicides is that they typically also affect crops which are exposed to the herbicide. One way to overcome this is to generate plants which are resistant to one or more broad-spectrum herbicides. Such herbicide-tolerant plants may reduce the need for tillage to control weeds, thereby effectively reducing soil erosion and can reduce the quantity and number of different herbicides applied in the field.

Common herbicides used, for example, include those that inhibit the enzyme 5-enolpyruvyl-3-phosphoshikimic acid synthase (EPSPS), for example N-phosphonomethyl-glycine (e.g. glyphosate), those that inhibit acetolactate synthase (ALS) activity, for example the sulfonylureas and related herbicides, and those that inhibit dihydropteroate synthase, for example methyl[(4-amino-phenyl)sulfonyl]carbamate (e.g. Asulam). Herbicide-tolerant plants can be produced by several methods, including, for example, introducing into the genome of the plant the ability to degrade the herbicide, the capacity to produce a higher level of the targeted enzyme, and/or expressing an herbicide-tolerant allele of the enzyme.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes that confer herbicide resistance.

Table 10
Genome-Altering Oligos Conferring Glyphosate Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Glyphosate Resistance EPSPS *Arabidopsis thaliana* Gly97Ala GGC-GCC	AAGCGTCGGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTC TTATTAAGCTTCCTG**C**CTCCAAGTCTCTATCAAATCGGATCCTGC TTCTCGCTGCTCTGTCTGAGGTATATATCAC	4341
	GTGATATATACCTCAGACAGAGCAGCGAGAAGCAGGATCCGATT TGATAGAGACTTGGAG**G**CAGGAAGCTTAATAAGACCGGAGATTT CTCTAATGGGTTGAAGTACAATCTCCGACGCTT	4342
	GCTTCCTG**C**CTCCAAGT	4343
	ACTTGGAG**G**CAGGAAGC	4344
Glyphosate Resistance EPSPS *Brassica napus* Gly93Ala GGA-GCA	AAGCTTCAGAGATTGTGCTTCAACCAATCAGAGAAATCTCGGGTC TCATTAAGCTACCCG**C**ATCCAAATCTCTCTCCAATCGGATCCTCC TTCTTGCCGCTCTATCTGAGGTACATATACT	4345
	AGTATATGTACCTCAGATAGAGCGGCAAGAAGGAGGATCCGATT GGAGAGAGATTTGGAT**G**CGGGTAGCTTAATGAGACCCGAGATTT CTCTGATTGGTTGAAGCACAATCTCTGAAGCTT	4346
	GCTACCCG**C**ATCCAAAT	4347
	ATTTGGAT**G**CGGGTAGC	4348
Glyphosate Resistance EPSPS 1 *Nicotiana tabacum* Gly95Ala GGT-GCT	AGCCCAACGAGATTGTGCTGCAACCCATCAAAGATATATCAGGC ACTGTTAAATTGCCTG**C**TTCTAAATCCCTTTCCAATCGTATTCTCC TTCTTGCTGCCCTTTCTAAGGGAAGGACTGT	4349
	ACAGTCCTTCCCTTAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTTAGAA**G**CAGGCAATTTAACAGTGCCTGATATATC TTTGATGGGTTGCAGCACAATCTCGTTGGGCT	4350
	ATTGCCTG**C**TTCTAAAT	4351
	ATTTAGAA**G**CAGGCAAT	4352
Glyphosate Resistance EPSPS 2 *Nicotiana tabacum* Gly62Ala GGA-GCA	ATTGTTTCCTTGGTACGAAATGTCCTCCTGTTCGAATTGTCAGCA AGGGAGGCCTTCCCG**C**AGGGAAGGTAAAGCTCTCTGGATCAATT AGCAGCCAGTACTTGACTGCTCTGCTTATGGC	4353
	GCCATAAGCAGAGCAGTCAAGTACTGGCTGCTAATTGATCCAGA GAGCTTTACCTTCCCT**G**CGGGAAGGCCTCCCTTGCTGACAATTC GAACAGGAGGACATTTCGTACCAAGGAAACAAT	4354
	CCTTCCCG**C**AGGGAAGG	4355
	CCTTCCCT**G**CGGGAAGG	4356
Glyphosate Resistance EPSPS *Zea mays* Gly168Ala GGT-GCT	ATTGTTTCCTTGGCACTGACTGCCCACCTGTTCGTGTCAATGGAA TCGGAGGGCTACCTG**C**TGGCAAGGTCAAGCTGTCTGGCTCCATC AGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	4357
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAGCCAGA CAGCTTGACCTTGCCA**G**CAGGTAGCCCTCCGATTCCATTGACAC GAACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	4358

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCTACCTG**C**TGGCAAGG	4359
	CCTTGCCA**G**CAGGTAGC	4360
Glyphosate Resistance EPSPS *Oryza sativa* Gly115Ala GGT-GCT	ACTGTTTCCTTGGCACTGAATGCCCACCTGTTCGTGTCAAGGGA ATTGGAGGACTTCCTG**C**TGGCAAGGTTAAGCTCTCTGGTTCCAT CAGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	4361
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAACCAGA GAGCTTAACCTTGCCAGCAGGAAGTCCTCCAATTCCCTTGACAC GAACAGGTGGGCATTCAGTGCCAAGGAAACAGT	4362
	ACTTCCTG**C**TGGCAAGG	4363
	CCTTGCCA**G**CAGGAAGT	4364
Glyphosate Resistance EPSPS *Petunia x hybrida* Gly93Ala GGC-GCC	AGCCTTCTGAGATAGTGTTGCAACCCATTAAAGAGATTTCAGGCA CTGTTAAATTGCCTG**C**CTCTAAATCATTATCTAATAGAATTCTCCT TCTTGCTGCCTTATCTGAAGGAACAACTGT	4365
	ACAGTTGTTCCTTCAGATAAGGCAGCAAGAAGGAGAATTCTATTA GATAATGATTTAGAG**G**CAGGCAATTTAACAGTGCCTGAAATCTCT TTAATGGGTTGCAACACTATCTCAGAAGGCT	4366
	ATTGCCTG**C**CTCTAAAT	4367
	ATTTAGAG**G**CAGGCAAT	4368
Glyphosate Resistance EPSPS *Lycopersicon esculentum* Gly97Ala GGT-GCT	AACCCCATGAGATTGTGCTAGNACCCATCAAAGATATATCTGGTA CTGTTAAATTACCCG**C**TTCGAAATCCCTTTCCAATCGTATTCTCCT TCTTGCTGCCCTTTCTGAGGGAAGGACTGT	4369
	ACAGTCCTTCCCTCAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTTCGAA**G**CGGGTAATTTAACAGTACCAGATATATC TTTGATGGGTNCTAGCACAATCTCATGGGGTT	4370
	ATTACCCG**C**TTCGAAAT	4371
	ATTTCGAA**G**CGGGTAAT	4372
Glyphosate Resistance EPSPS *Lolium rigidum* Gly107Ala GGT-GCT	ATTGTTTCCTTGGCACTGACTGCCCACCTGTTCGKATCAACGGCA TTGGAGGGCTACCTG**C**TGGCAAGGTTAAGCTGTCTGGTTCCATC AGCAGCCAATACTTGAGTTCCTTGCTGATGGC	4373
	GCCATCAGCAAGGAACTCAAGTATTGGCTGCTGATGGAACCAGA CAGCTTAACCTTGCCA**G**CAGGTAGCCCTCCAATGCCGTTGATCG AACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	4374
	GCTACCTG**C**TGGCAAGG	4375
	CCTTGCCA**G**CAGGTAGC	4376

Table 11

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS *Arabidopsis thaliana* Pro197Ser CCT-TCT	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCAATCACAGGACAAGTC**T**CTCGTCGTATGATTGGTACAGATGCGTTTCAAGAGACTCCGATTGTTGAGGTAACGCGTT	4377
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTACCAATCATACGACGAG**A**GACTTGTCCTGTGATTGCTACAAGAGGAACACTATCTAACAACGCATCGGCTAATCCGCT	4378
	GACAAGTC**T**CTCGTCGT	4379
	ACGACGAG**A**GACTTGTC	4380
Sulfonylurea Resistance ALS *Arabidopsis thaliana* Pro197Gln CCT-CAG	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCAATCACAGGACAAGTCC**AG**CGTCGTATGATTGGTACAGATGCGTTTCAAGAGACTCCGATTGTTGAGGTAACGCGTT	4381
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTACCAATCATACGACG**CT**GGACTTGTCCTGTGATTGCTACAAGAGGAACACTATCTAACAACGCATCGGCTAATCCGCT	4382
	ACAAGTCC**AG**CGTCGTC	4383
	TACGACG**CT**GGACTTGT	4384
Sulfonylurea Resistance ALS *Arabidopsis thaliana* Pro197Gln CCT-CAA	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCAATCACAGGACAAGTCC**AA**CGTCGTATGATTGGTACAGATGCGTTTCAAGAGACTCCGATTGTTGAGGTAACGCGTT	4385
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTACCAATCATACGACG**TT**GGACTTGTCCTGTGATTGCTACAAGAGGAACACTATCTAACAACGCATCGGCTAATCCGCT	4386
	ACAAGTCC**AA**CGTCGTA	4387
	TACGACG**TT**GGACTTGT	4388
Imidazolinone Resistance ALS *Arabidopsis thaliana* Ser653Asn AGT-AAC	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGTTGCCGATGATCCCGA**AC**GGTGGCACTTTCAACGATGTCATAACGGAAGGAGATGGCCGGATTAAATACTGAGAGAT	4389
	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGTTGAAAGTGCCACC**GT**TCGGGATCATCGGCAACACATGTTCTTGGTGCGGACAAATCACATCCAACAGGTAAGGTC	4390
	GATCCCGA**AC**GGTGGCA	4391
	TGCCACC**GT**TCGGGATC	4392

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Imidazolinone Resistance ALS *Arabidopsis thaliana* Ser653Asn AGT-AAT	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGA**AT**GGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4393
	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACC**AT**TCGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	4394
	GATCCCGA**AT**GGTGGCA	4395
	TGCCACC**AT**TCGGGATC	4396
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCG CCATCACGGGCCAGGTC**T**CCCGCCGCATGATCGGCACCGACGC CTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	4397
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGG**A**GACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	4398
	GCCAGGTC**T**CCCGCCGC	4399
	GCGGCGGG**A**GACCTGGC	4400
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAA	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCC**AA**CGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4401
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCG**TT**GGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4402
	CCAGGTCC**AA**CGCCGCA	4403
	TGCGGCG**TT**GGACCTGG	4404
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAG	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCC**AG**CGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4405
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCG**CT**GGACCTGGCCCGTGATGGCGACCATC GGGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4406
	CCAGGTCC**AG**CGCCGCA	4407
	TGCGGCG**CT**GGACCTGG	4408
Imidazolinone Resistance ALS *Oryza sativa* Ile627Asn ATT-AAT	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCCTATGATCCCAA**A**TGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4409
	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCA**T**TTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC	4410
	GATCCCAA**A**TGGGGGCG	4411

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCCCCCA**T**TTGGGATC	4412
Sulfonylurea Resistance ALS *Zea mays* Pro165Ser CCG-TCG	TCCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGC CATCACGGGACAGGTG**T**CGCGACGCATGATTGGCACCGACGCCT TCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4413
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGGT GCCAATCATGCGTCGCG**A**CACCTGTCCCGTGATGGCGACCATGG GGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	4414
	GACAGGTG**T**CGCGACGC	4415
	GCGTCGCG**A**CACCTGTC	4416
Sulfonylurea Resistance ALS *Zea mays* Pro165Gln CCG-CAG	CCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGCC ATCACGGGACAGGTGC**A**GCGACGCATGATTGGCACCGACGCCTT CCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4417
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGG TGCCAATCATGCGTCGC**T**GCACCTGTCCCGTGATGGCGACCATG GGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGG	4418
	ACAGGTGC**A**GCGACGCA	4419
	TGCGTCGC**T**GCACCTGT	4420
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAT	GGCCGTACCTCTTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTA**AT**GGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4421
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT TGAAAGCCCCACC**AT**TAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4422
	GATCCCTA**AT**GGTGGGG	4423
	CCCCACC**AT**TAGGGATC	4424
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAC	GGCCGTACCTCTTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTA**AC**GGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4425
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT TGAAAGCCCCACC**GT**TAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4426
	GATCCCTA**AC**GGTGGGG	4427
	CCCCACC**GT**TAGGGATC	4428
Sulfonylurea Resistance ALS *Lolium multiflorum* Pro167Ser CCG-TCG	TCCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGC CATCACGGGGCAGGTC**T**CGCGCCGCATGATCGGCACGGACGCC TTCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4429
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGT GCCGATCATGCGGCGCG**A**GACCTGCCCCGTGATGGCCACCATG GGGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGGA	4430

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGCAGGTC**T**CGCGCCGC	4431
	GCGGCGCG**A**GACCTGCC	4432
Sulfonylurea Resistance ALS *Lolium multiflorum* Pro167Gln CCG-CAG	CCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGCCATCACGGGGCAGGTCC**A**GCGCCGCATGATCGGCACGGACGCCTTCCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4433
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGTGCCGATCATGCGGCGC**T**GGACCTGCCCCGTGATGGCCACCATGGGGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGG	4434
	GCAGGTCC**A**GCGCCGCA	4435
	TGCGGCGC**T**GGACCTGC	4436
Imidazolinone Resistance ALS *Lolium multiflorum* Ser623Asn AGC-AAC	CTGGGCCATACTTGTTGGATATCATCGTCCCTCACCAGGAGCATGTGCTGCCTATGATCCCTA**A**CGGTGGTGCTTTCAAGGACATTATCATGGAAGGTGATGGCAGGATTTCGTATTAAAC	4437
	GTTTAATACGAAATCCTGCCATCACCTTCCATGATAATGTCCTTGAAAGCACCACCG**T**TAGGGATCATAGGCAGCACATGCTCCTGGTGAGGGACGATGATATCCAACAAGTATGGCCCAG	4438
	GATCCCTA**A**CGGTGGTG	4439
	CACCACCG**T**TAGGGATC	4440
Sulfonylurea Resistance ALS *Hordeum vulgare* Pro68Ser CCA-TCA	TCCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGCCATCACGGGCCAGGTC**T**CACGCCGCATGATCGGCACGGACGCGTTCCAGGAGACGCCCATAGTGGAGGTCACGCGCT	4441
	AGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGTGCCGATCATGCGGCGTG**A**GACCTGGCCCGTGATGGCGACCATGGGGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGGA	4442
	GCCAGGTC**T**CACGCCGC	4443
	GCGGCGTG**A**GACCTGGC	4444
Sulfonylurea Resistance ALS *Hordeum vulgare* Pro68Gln CCA-CAA	CCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGCCATCACGGGCCAGGTCC**A**ACGCCGCATGATCGGCACGGACGCGTTCCAGGAGACGCCCATAGTGGAGGTCACGCGCTC	4445
	GAGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGTGCCGATCATGCGGCGT**T**GGACCTGGCCCGTGATGGCGACCATGGGGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGG	4446
	CCAGGTCC**A**ACGCCGCA	4447
	TGCGGCGT**T**GGACCTGG	4448

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Imidazolinone Resistance ALS *Hordeum vulgare* Ser524Asn AGC-AAC	CCCAGGGCCGTACCTGCTGGATATCATTGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAA**A**CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGTACTGA	4449
	TCAGTACGAGGTCCTGCCATCACCCTCCATGATCATGTCCTTGAAAGCACCACCG**T**TTGGGATCATAGGCAGCACGTGCTCCTGATGCGGGACAATGATATCCAGCAGGTACGGCCCTGGG	4450
	GATCCCAA**A**CGGTGGTG	4451
	CACCACCG**T**TTGGGATC	4452
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGATCACTGGTCAAGTC**T**CTCGTCGGATGATCGGTACCGATGCTTTCCAGGAAACTCCAATTGTTGAGGTAACAAGGT	4453
	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTACCGATCATCCGACGAG**A**GACTTGACCAGTGATCGCCACGAGAGGGATACTATCGAGCATTGCATCAGCGAGACCACT	4454
	GTCAAGTC**T**CTCGTCGG	4455
	CCGACGAG**A**GACTTGAC	4456
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGATCACTGGTCAAGTCC**AA**CGTCGGATGATCGGTACCGATGCTTTCCAGGAAACTCCAATTGTTGAGGTAACAAGGTC	4457
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTACCGATCATCCGACG**TT**GGACTTGACCAGTGATCGCCACGAGAGGGATACTATCGAGCATTGCATCAGCGAGACCAC	4458
	TCAAGTCC**AA**CGTCGGA	4459
	TCCGACG**TT**GGACTTGA	4460
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGATCACTGGTCAAGTCC**AG**CGTCGGATGATCGGTACCGATGCTTTCCAGGAAACTCCAATTGTTGAGGTAACAAGGTC	4461
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTACCGATCATCCGACG**CT**GGACTTGACCAGTGATCGCCACGAGAGGGATACTATCGAGCATTGCATCAGCGAGACCAC	4462
	TCAAGTCC**AG**CGTCGGA	4463
	TCCGACG**CT**GGACTTGA	4464
Imidazolinone Resistance ALS *Gossypium hirsutum* Ser642Asn AGT-AAT	GACCTTACTTGTTGGATGTGATTGTCCCACATCAAGAACATGTCCTGCCTATGATCCCCA**A**TGGAGGCGCTTTCAAAGATGTGATCACAGAGGGTGATGGAAGAACACAATATTGACCTCA	4465
	TGAGGTCAATATTGTGTTCTTCCATCACCCTCTGTGATCACATCTTTGAAAGCGCCTCCA**T**TGGGGATCATAGGCAGGACATGTTCTTGATGTGGGACAATCACATCCAACAAGTAAGGTC	4466
	GATCCCCA**A**TGGAGGCG	4467

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCCTCCA**T**TGGGGATC	4468
Sulfonylurea Resistance ALS *Amaranthus retroflexus* Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCC ATTACTGGGCAAGTT**T**CCCGGCGTATGATTGGTACTGATGCTTTTC AAGAGACTCCAATTGTTGAGGTAACTCGAT	4469
	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC AATCATACGCCGGG**A**AACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4470
	GGCAAGTT**T**CCCGGCGT	4471
	ACGCCGGG**A**AACTTGCC	4472
Sulfonylurea Resistance ALS *Amaranthus retroflexus* Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTTC**AA**CGGCGTATGATTGGTACTGATGCTTTTC AAGAGACTCCAATTGTTGAGGTAACTCGATC	4473
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG**TT**GAACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAG	4474
	GCAAGTTC**AA**CGGCGTA	4475
	TACGCCG**TT**GAACTTGC	4476
Sulfonylurea Resistance ALS *Amaranthus retroflexus* Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTTC**AG**CGGCGTATGATTGGTACTGATGCTTTTC AAGAGACTCCAATTGTTGAGGTAACTCGATC	4477
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG**CT**GAACTTGCCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4478
	GCAAGTTC**AG**CGGCGTA	4479
	TACGCCG**CT**GAACTTGC	4480
Imidazolinone Resistance ALS *Amaranthus retroflexus* Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC TGCCTATGATCCCTA**A**CGGTGCCGCCTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4481
	ACCAACTAATAAGCCCTTCTTCCATCACCCTCTGTTATGGTGTCCT TGAAGGCGGCACCG**T**TAGGGATCATAGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATACGGTC	4482
	GATCCCTA**A**CGGTGCCG	4483
	CGGCACCG**T**TAGGGATC	4484

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS 1 *Nicotiana tabacum* Pro194Ser CCA-TCA	AGCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGC TATAACAGGTCAAGTGTCACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAACTAGAT	4485
	ATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTACC TATCATCCTACGTGACACTTGACCTGTTATAGCAACAATGGGGAC GCTATCCAGTAGCGCGTCAGCGAGGCCGCT	4486
	GTCAAGTGTCACGTAGG	4487
	CCTACGTGACACTTGAC	4488
Sulfonylurea Resistance ALS 1 *Nicotiana tabacum* Pro194Gln CCA-CAA	GCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGCT ATAACAGGTCAAGTGCAACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAACTAGATC	4489
	GATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTAC CTATCATCCTACGTTGCACTTGACCTGTTATAGCAACAATGGGGA CGCTATCCAGTAGCGCGTCAGCGAGGCCGC	4490
	TCAAGTGCAACGTAGGA	4491
	TCCTACGTTGCACTTGA	4492
Imidazolinone Resistance ALS 1 *Nicotiana tabacum* Ser650Asn AGT-AAT	GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTTT ACCTATGATTCCCAATGGCGGAGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAGTTCCTATTGAGTTTG	4493
	CAAACTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCTCCGCCATTGGGAATCATAGGTAAAACATGTTCCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4494
	GATTCCCAATGGCGGAG	4495
	CTCCGCCATTGGGAATC	4496
Sulfonylurea Resistance ALS 2 *Nicotiana tabacum* Pro191Ser CCA-TCA	AGTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGC TATAACCGGTCAAGTGTCACGTAGGATGATCGGTACTGATGCTTTT CAGGAAACTCCGATTGTTGAGGTAACTAGAT	4497
	ATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTACC GATCATCCTACGTGACACTTGACCGGTTATAGCAACAATGGGGAC GCTATCCAGTAGGGCGTCCGCGAGGCCACT	4498
	GTCAAGTGTCACGTAGG	4499
	CCTACGTGACACTTGAC	4500
Sulfonylurea Resistance ALS 2 *Nicotiana tabacum* Pro191Gln CCA-CAA	GTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGCT ATAACCGGTCAAGTGCAACGTAGGATGATCGGTACTGATGCTTTT CAGGAAACTCCGATTGTTGAGGTAACTAGATC	4501
	GATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTAC CGATCATCCTACGTTGCACTTGACCGGTTATAGCAACAATGGGGA CGCTATCCAGTAGGGCGTCCGCGAGGCCAC	4502
	TCAAGTGCAACGTAGGA	4503

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCTACGT**T**GCACTTGA	4504
Imidazolinone Resistance ALS 2 *Nicotiana tabacum* Ser647Asn AGT-AAT	GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTCT ACCTATGATTCCCA**A**TGGCGGGGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAGTTCCTATTGACTTTG	4505
	CAAAGTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCCCCGCCA**T**TGGGAATCATAGGTAGAACATGTTCCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4506
	GATTCCCA**A**TGGCGGGG	4507
	CCCCGCCA**T**TGGGAATC	4508
Sulfonylurea Resistance ALS *Xanthium* spp. Pro175Ser CCC-TCC	AGTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTA TTACTGGTCAAGTT**T**CCAGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTT	4509
	AACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCC AATCATTCTCCTGG**A**AACTTGACCAGTAATAGCAACCATTGGAACA CTGTCTAATAAAGCATCAGCAAGACCACT	4510
	GTCAAGTT**T**CCAGGAGA	4511
	TCTCCTGG**A**AACTTGAC	4512
Sulfonylurea Resistance ALS *Xanthium* spp. Pro175Gln CCC-CAA	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT TACTGGTCAAGTTC**AA**AGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTTC	4513
	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTC CAATCATTCTCCT**TT**GAACTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC	4514
	TCAAGTTC**AA**AGGAGAA	4515
	TTCTCCT**TT**GAACTTGA	4516
Sulfonylurea Resistance ALS *Xanthium* spp. Pro175Gln CCC-CAG	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT TACTGGTCAAGTTC**AG**AGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTTC	4517
	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTC CAATCATTCTCCT**CT**GAACTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC	4518
	TCAAGTTC**AG**AGGAGAA	4519
	TTCTCCT**CT**GAACTTGA	4520
Imidazolinone Resistance ALS *Xanthium* spp. Ala631Asn GCT-AAT	GGGCCTTACTTGTTGGATGTGATCGTGCCCCATCAAGAACATGTG TTGCCCATGATCCCG**AA**TGGTGGAGGTTTCATGGATGTGATCACC GAAGGCGACGGCAGAATGAAATATTGAGCTT	4521
	AAGCTCAATATTTCATTCTGCCGTCGCCTTCGGTGATCACATCCAT GAAACCTCCACCA**TT**CGGGATCATGGGCAACACATGTTCTTGATG GGGCACGATCACATCCAACAAGTAAGGCCC	4522

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATCCCG**AA**TGGTGGA	4523
	TCCACCA**TT**CGGGATCA	4524
Sulfonylurea Resistance ALS *Bassia scoparia* Pro189Ser CCG-TCG	TCCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCG ATCACGGGGCAGGTG**T**CGCGGCGAATGATTGGGACGGATGCTTT TCAGGAGACTCCTATTGTTGAGGTAACACGGT	4525
	ACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTCC CAATCATTCGCCGCG**A**CACCTGCCCCGTGATCGCCACCAGTGGA ACGGAATCGAGCAAAGCATCAGCAAACCCGGA	4526
	GGCAGGTG**T**CGCGGCGA	4527
	TCGCCGCG**A**CACCTGCC	4528
Sulfonylurea Resistance ALS *Bassia scoparia* Pro189Gln CCG-CAG	CCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCGA TCACGGGGCAGGTGC**A**GCGGCGAATGATTGGGACGGATGCTTTT CAGGAGACTCCTATTGTTGAGGTAACACGGTC	4529
	GACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTC CCAATCATTCGCCGC**T**GCACCTGCCCCGTGATCGCCACCAGTGG AACGGAATCGAGCAAAGCATCAGCAAACCCGG	4530
	GCAGGTGC**A**GCGGCGAA	4531
	TTCGCCGC**T**GCACCTGC	4532
Imidazolinone Resistance ALS *Bassia scoparia* Ser649Asn AGT-AAT	GACCTTACCTGCTTGATGTGATTGTACCTCATCAGGAGCATGTGC TGCCTATGATTCCTA**A**TGGTGCAGCCTTCAAGGATATCATTAACGA AGGTGATGGAAGAACAAGTTATTGATGTTC	4533
	GAACATCAATAACTTGTTCTTCCATCACCTTCGTTAATGATATCCTT GAAGGCTGCACCA**T**TAGGAATCATAGGCAGCACATGCTCCTGATG AGGTACAATCACATCAAGCAGGTAAGGTC	4534
	GATTCCTA**A**TGGTGCAG	4535
	CTGCACCA**T**TAGGAATC	4536
Sulfonylurea Resistance ALS 1 *Brassica napus* Pro182Ser CCT-TCT	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGC CATTACAGGACAGGTC**T**CTCGCCGGATGATCGGTACTGACGCCTT CCAAGAGACACCAATCGTTGAGGTAACGAGGT	4537
	ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTAC CGATCATCCGGCGAG**A**GACCTGTCCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	4538
	GACAGGTC**T**CTCGCCGG	4539
	CCGGCGAG**A**GACCTGTC	4540

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS 1 *Brassica napus* Pro182Gln CCT-CAA	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCATTACAGGACAGGTCC**AA**CGCCGGATGATCGGTACTGACGCCTTCCAAGAGACACCAATCGTTGAGGTAACGAGGTC	4541
	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACCGATCATCCGGCG**TT**GGACCTGTCCTGTAATGGCGACAAGAGGAACACTGTCAAGCATCGCGTCTGCTAACCCGC	4542
	ACAGGTCC**AA**CGCCGGA	4543
	TCCGGCG**TT**GGACCTGT	4544
Sulfonylurea Resistance ALS 1 *Brassica napus* Pro182Gln CCT-CAG	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCATTACAGGACAGGTCC**AG**CGCCGGATGATCGGTACTGACGCCTTCCAAGAGACACCAATCGTTGAGGTAACGAGGTC	4545
	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACCGATCATCCGGCG**CT**GGACCTGTCCTGTAATGGCGACAAGAGGAACACTGTCAAGCATCGCGTCTGCTAACCCGC	4546
	ACAGGTCC**AG**CGCCGGA	4547
	TCCGGCG**CT**GGACCTGT	4548
Imidazolinone Resistance ALS 1 *Brassica napus* Ser638Asn AGT-AAT	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGTTACCGATGATCCCAA**A**TGGTGGCACTTTCAAAGATGTAATAACAGAAGGGGATGGTCGCACTAAGTACTGAGAGAT	4549
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCTGTTATTACATCTTTGAAAGTGCCACCA**T**TTGGGATCATCGGTAACACATGTTCTTGGTGCGGACATATCACATCCAACAGGTATGGTC	4550
	GATCCCAA**A**TGGTGGCA	4551
	TGCCACCA**T**TTGGGATC	4552
Sulfonylurea Resistance ALS 2 *Brassica napus* Pro126Ser CCC-TCC	CAGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCATTACAGGACAGGT**T**CCTCGCCGGATGATCGGTACTGACGCCTTCCAAGAGACACCAATCGTTGAGGTAACGAGG	4553
	CCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACCGATCATCCGGCGAGG**A**ACCTGTCCTGTAATGGCGACAAGAGGAACACTGTCAAGCATCGCGTCTGCTAACCCGCTG	4554
	GGACAGGT**T**CCTCGCCG	4555
	CGGCGAGG**A**ACCTGTCC	4556
Sulfonylurea Resistance ALS 2 *Brassica napus* Pro126Gln CCC-CAG	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCATTACAGGACAGGTC**A**CTCGCCGGATGATCGGTACTGACGCCTTCCAAGAGACACCAATCGTTGAGGTAACGAGGT	4557
	ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACCGATCATCCGGCGAG**T**GACCTGTCCTGTAATGGCGACAAGAGGAACACTGTCAAGCATCGCGTCTGCTAACCCGCT	4558
	GACAGGTC**A**CTCGCCGG	4559

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGGCGAG**T**GACCTGTC	4560
Imidazolinone Resistance ALS 2 *Brassica napus* Ser582Asn AGT-AAT	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA**A**TGGTGGCACTTTCAAAGATGTAATAACAGA AGGGGATGGTCGCACTAAGTACTGAGAGAT	4561
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCTGTTATTACATCTT TGAAAGTGCCACCA**T**TTGGGATCATCGGTAACACATGTTCTTGGT GCGGACATATCACATCCAACAGGTATGGTC	4562
	GATCCCAA**A**TGGTGGCA	4563
	TGCCACCA**T**TTGGGATC	4564
Sulfonylurea Resistance ALS 3 *Brassica napus* Pro179Ser CCT-TCT	AGCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGC CATCACAGGACAGGTC**T**CTCGCCGGATGATCGGTACTGACGCGT TCCAAGAGACGCCAATCGTTGAGGTAACGAGGT	4565
	ACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTAC CGATCATCCGGCGAG**A**GACCTGTCCTGTGATGGCGACGAGAGGA ACACTGTCAAGCATCGCGTCGGCTAACCCGCT	4566
	GACAGGTC**T**CTCGCCGG	4567
	CCGGCGAG**A**GACCTGTC	4568
Sulfonylurea Resistance ALS 3 *Brassica napus* Pro179Gln CCT-CAA	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGCC ATCACAGGACAGGTCC**AA**CGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	4569
	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCG**TT**GGACCTGTCCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGTCGGCTAACCCGC	4570
	ACAGGTCC**AA**CGCCGGA	4571
	TCCGGCG**TT**GGACCTGT	4572
Sulfonylurea Resistance ALS 3 *Brassica napus* Pro179Gln CCT-CAG	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGCC ATCACAGGACAGGTCC**AG**CGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	4573
	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCG**CT**GGACCTGTCCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGTCGGCTAACCCGC	4574
	ACAGGTCC**AG**CGCCGGA	4575
	TCCGGCG**CT**GGACCTGT	4576
Imidazolinone Resistance ALS 3 *Brassica napus* Ser635Asn AGT-AAT	GACCGTACCTGTTGGATGTCATCTGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA**A**TGGTGGCACTTTCAAAGATGTAATAACCG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	4577
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCGGTTATTACATCTT TGAAAGTGCCACCA**T**TTGGGATCATCGGTAACACATGTTCTTGGT GCGGACAGATGACATCCAACAGGTACGGTC	4578

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GATCCCAA**A**TGGTGGCA	4579
	TGCCACCA**T**TTGGGATC	4580
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCG CCATCACGGGCCAGGTC**T**CCCGCCGCATGATCGGCACCGACGC CTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	4581
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGG**A**GACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	4582
	GCCAGGTC**T**CCCGCCGC	4583
	GCGGCGGG**A**GACCTGGC	4584
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAA	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCC**AA**CGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4585
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCG**TT**GGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4586
	CCAGGTCC**AA**CGCCGCA	4587
	TGCGGCG**TT**GGACCTGG	4588
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAG	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCC**AG**CGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4589
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCG**CT**GGACCTGGCCCGTGATGGCGACCATC GGGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4590
	CCAGGTCC**AG**CGCCGCA	4591
	TGCGGCG**CT**GGACCTGG	4592
Imidazolinone Resistance ALS *Oryza sativa* Ser627Asn AGT-AAT	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCCTATGATCCCAA**A**TGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4593
	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCA**T**TTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC	4594
	GATCCCAA**A**TGGGGGCG	4595
	CGCCCCCA**T**TTGGGATC	4596

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS *Zea mays* Pro165Ser CCG-TCG	TCTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGCCATCACGGGACAGGTG**T**CGCGACGCATGATTGGCACCGACGCCTTTCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4597
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGTGCCAATCATGCGTCGCG**A**CACCTGTCCCGTGATGGCGACCATGGGGACGGAGTCGAGCAACGCGTCTGCGAGCGCAGA	4598
	GACAGGTG**T**CGCGACGC	4599
	GCGTCGCG**A**CACCTGTC	4600
Sulfonylurea Resistance ALS *Zea mays* Pro165Gln CCG-CAG	CTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGCCATCACGGGACAGGTGC**A**GCGACGCATGATTGGCACCGACGCCTTTCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4601
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGTGCCAATCATGCGTCGC**T**GCACCTGTCCCGTGATGGCGACCATGGGGACGGAGTCGAGCAACGCGTCTGCGAGCGCAG	4602
	ACAGGTGC**A**GCGACGCA	4603
	TGCGTCGC**T**GCACCTGT	4604
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAT	GGCCGTACCTCTTGGATATAATCGTCCCGCACCAGGAGCATGTGTTGCCTATGATCCCTA**A**TGGTGGGGCTTTCAAGGATATGATCCTGGATGGTGATGGCAGGACTGTGTATTGATCCGT	4605
	ACGGATCAATACACAGTCCTGCCATCACCATCCAGGATCATATCCTTGAAAGCCCCACCA**T**TAGGGATCATAGGCAACACATGCTCCTGGTGCGGGACGATTATATCCAAGAGGTACGGCC	4606
	GATCCCTA**A**TGGTGGGG	4607
	CCCCACCA**T**TAGGGATC	4608
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGATCACTGGTCAAGTC**T**CTCGTCGGATGATCGGTACCGATGCTTTCCAGGAAACTCCAATTGTTGAGGTAACAAGGT	4609
	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTACCGATCATCCGACGAG**A**GACTTGACCAGTGATCGCCACGAGAGGGATACTATCGAGCATTGCATCAGCGAGACCACT	4610
	GTCAAGTCTC**T**CGTCGG	4611
	CCGACGAGAG**A**CTTGAC	4612
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGATCACTGGTCAAGTCC**AA**CGTCGGATGATCGGTACCGATGCTTTCCAGGAAACTCCAATTGTTGAGGTAACAAGGTC	4613
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTACCGATCATCCGACG**TT**GGACTTGACCAGTGATCGCCACGAGAGGGATACTATCGAGCATTGCATCAGCGAGACCAC	4614
	TCAAGTCC**AA**CGTCGGA	4615

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACG**TT**GGACTTGA	4616
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGATCACTGGTCAAGTCC**AG**CGTCGGATGATCGGTACCGATGCTTTCCAGGAAACTCCAATTGTTGAGGTAACAAGGTC	4617
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTACCGATCATCCGACG**CT**GGACTTGACCAGTGATCGCCACGAGAGGGATACTATCGAGCATTGCATCAGCGAGACCAC	4618
	TCAAGTCC**AG**CGTCGGA	4619
	TCCGACG**CT**GGACTTGA	4620
Imidazolinone Resistance ALS *Gossypium hirsutum* Ser642Asn AGT-AAT	GACCTTACTTGTTGGATGTGATTGTCCCACATCAAGAACATGTCCTGCCTATGATCCCCA**A**TGGAGGGGCTTTCAAAGATGTGATCACAGAGGGTGATGGAAGAACACAATATTGACCTCA	4621
	TGAGGTCAATATTGTGTTCTTCCATCACCCTCTGTGATCACATCTTTGAAAGCCCCTCCA**T**TGGGGATCATAGGCAGGACATGTTCTTGATGTGGGACAATCACATCCAACAAGTAAGGTC	4622
	GATCCCCA**A**TGGAGGGG	4623
	CCCCTCCA**T**TGGGGATC	4624
Sulfonylurea Resistance ALS *Amaranthus powellii* Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCATTACTGGGCAAGTT**T**CCCGGCGTATGATTGGTACTGATGCTTTTCAAGAGACTCCAATTGTTGAGGTAACTCGAT	4625
	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACCAATCATACGCCGGG**A**AACTTGCCCAGTAATGGCGACAAGAGGGACTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4626
	GGCAAGTT**T**CCCGGCGT	4627
	ACGCCGGG**A**AACTTGCC	4628
Sulfonylurea Resistance ALS *Amaranthus powellii* Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCATTACTGGGCAAGTTC**AA**CGGCGTATGATTGGTACTGATGCTTTTCAAGAGACTCCAATTGTTGAGGTAACTCGATC	4629
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACCAATCATACGCCG**TT**GAACTTGCCCAGTAATGGCGACAAGAGGGACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4630
	GCAAGTTC**AA**CGGCGTA	4631
	TACGCCG**TT**GAACTTGC	4632
Sulfonylurea Resistance ALS *Amaranthus powellii* Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCATTACTGGGCAAGTTC**AG**CGGCGTATGATTGGTACTGATGCTTTTCAAGAGACTCCAATTGTTGAGGTAACTCGATC	4633
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACCAATCATACGCCG**CT**GAACTTGCCCAGTAATGGCGACAAGAGGGACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4634

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCAAGTTC**AG**CGGCGTA	4635
	TACGCCG**CT**GAACTTGC	4636
Imidazolinone Resistance ALS *Amaranthus powellii* Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGCTGCCTATGATCCCTA**A**CGGTGCCGCCTTCAAGGACACCATAACAGAGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4637
	ACCAACTAATAAGCCCTTCTTCCATCACCCTCTGTTATGGTGTCCTTGAAGGCGGCACCGTTAGGGATCATAGGCAGCACATGCTCCTGATGTGGTACGATTACATCCAGCAGATACGGTC	4638
	GATCCCTAACGGTGCCG	4639
	CGGCACCGTTAGGGATC	4640

Table 12
Genome-Altering Oligos Conferring Porphyric Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Porphyric Herbicide Resistant PPO *Arabidopsis thaliana* Val365Met GTT-ATG	TCTTGCGCCCTCTTTCTGAATCTGCTGCAAATGCACTCTCAAAACTATATTACCCACCA**A**T**G**GCAGCAGTATCTATCTCGTACCCGAAAGAAGCAATCCGAACAGAATGTTTGATAGATGG	4641
	CCATCTATCAAACATTCTGTTCGGATTGCTTCTTTCGGGTACGAGATAGATACTGCTGC**C**CA**T**TGGTGGGTAATATAGTTTTGAGAGTGCATTTGCAGCAGATTCAGAAAGAGGGCGCAAGA	4642
	CCCACCA**A**T**G**GCAGCAG	4643
	CTGCTGC**C**A**T**TGGTGGG	4644
Porphyric Herbicide Resistant PPO *Nicotiana tabacum* Val376Met GTT-ATG	TATTACGTCCTCTTTCGGTTGCCGCAGCAGATGCACTTTCAAATTTCTACTATCCCCCA**A**T**G**GGAGCAGTCACAATTTCATATCCTCAAGAAGCTATTCGTGATGAGCGTCTGGTTGATGG	4645
	CCATCAACCAGACGCTCATCACGAATAGCTTCTTGAGGATATGAAATTGTGACTGCTCC**C**A**T**TGGGGGATAGTAGAAATTTGAAAGTGCATCTGCTGCGGCAACCGAAAGAGGACGTAATA	4646
	TCCCCCA**A**T**G**GGAGCAG	4647
	CTGCTCC**C**A**T**TGGGGGA	4648
Porphyric Herbicide Resistant PPO *Cichorium intybus* Val383Met GTT-ATG	TGTTGCGTCCGCTTTCGTTGGGTGCAGCAGATGCATTGTCAAAATTTTATTATCCTCCG**A**T**G**GCAGCTGTATCAATTTCATATCCAAAAGACGCAATTCGTGCTGACCGGCTGATTGATGG	4649
	CCATCAATCAGCCGGTCAGCACGAATTGCGTCTTTTGGATATGAAATTGATACAGCTGC**C**A**T**CGGAGGATAATAAAATTTTGACAATGCATCTGCTGCACCCAACGAAAGCGGACGCAACA	4650
	TCCTCCG**A**T**G**GCAGCTG	4651
	CAGCTGC**C**A**T**CGGAGGA	4652
Porphyric Herbicide Resistant PPO *Spinacia oleracea* Val390Met GTT-ATG	TCCTTCGTCCACTTTCAGATGTCGCCGCAGAATCTCTTTCAAAATTTCATTATCCACCA**A**T**G**GCAGCTGTGTCACTTTCCTATCCTAAAGAAGCAATTAGATCAGAGTGCTTGATTGACGG	4653
	CCGTCAATCAAGCACTCTGATCTAATTGCTTCTTTAGGATAGGAAAGTGACACAGCTGC**C**A**T**TGGTGGATAATGAAATTTTGAAAGAGATTCTGCGGCGACATCTGAAAGTGGACGAAGGA	4654
	TCCACCA**A**T**G**GCAGCTG	4655
	CAGCTGC**C**A**T**TGGTGGA	4656

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Porphyric Herbicide Resistant PPO *Zea mays* Val363Met GTT-ATG	TTTTGCGTCCACTTTCAAGCGATGCTGCAGATGCTCTATCAAGATTCTATTATCCACCG**A**T**G**GCTGCTGTAACTGTTTCGTATCCAAAGGAAGCAATTAGAAAAGAATGCTTAATTGATGG	4657
	CCATCAATTAAGCATTCTTTTCTAATTGCTTCCTTTGGATACGAAACAGTTACAGCAGC**C**A**T**CGGTGGATAATAGAATCTTGATAGAGCATCTGCAGCATCGCTTGAAAGTGGACGCAAAA	4658
	TCCACCG**A**T**G**GCTGCTG	4659
	CAGCAGC**C**A**T**CGGTGGA	4660
Porphyric Herbicide Resistant PPO *Oryza sativa* Val364Met GTT-ATG	TCTTGCGGCCACTTTCAAGTGATGCAGCAGATGCTCTGTCAATATTCTATTATCCACCA**A**T**G**GCTGCTGTAACTGTTTCATATCCAAAAGAAGCAATTAGAAAAGAATGCTTAATTGACGG	4661
	CCGTCAATTAAGCATTCTTTTCTAATTGCTTCTTTTGGATATGAAACAGTTACAGCAGC**C**A**T**TGGTGGATAATAGAATATTGACAGAGCATCTGCTGCATCACTTGAAAGTGGCCGCAAGA	4662
	TCCACCA**A**T**G**GCTGCTG	4663
	CAGCAGC**C**A**T**TGGTGGA	4664
Porphyric Herbicide Resistant PPO *Chlamydomonas reinhardtii* Val389Met GTG-ATG	CTGGTCAAGGAGCAGGCGCCCGCCGCCGCCGAGGCCCTGGGCTCCTTCGACTACCCGCCG**A**TGGGCGCCGTGACGCTGTCGTACCCGCTGAGCGCCGTGCGGGAGGAGCGCAAGGCCTCGG	4665
	CCGAGGCCTTGCGCTCCTCCCGCACGGCGCTCAGCGGGTACGACAGCGTCACGGCGCCCA**T**CGGCGGGTAGTCGAAGGAGCCCAGGGCCTCGGCGGCGGCGGGCGCCTGCTCCTTGACCAG	4666
	ACCCGCCG**A**TGGGCGCC	4667
	GGCGCCCA**T**CGGCGGGT	4668

Table 13

Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Arabidopsis thaliana* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATTTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4669
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAAATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4670

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATATGCTA**C**TTTCAACA	4671
	TGTTGAAA**G**TAGCATAT	4672
Triazine Resistant D1 Protein *Nicotiana tabacum* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4673
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATGTTATAAGTTT	4674
	ATATGCTA**C**TTTCAACA	4675
	TGTTGAAA**G**TAGCATAT	4676
Triazine Resistant D1 Protein *Populus deltoides* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTTAACAACTCTCGCTCTTTACATTTCTTCTTAGCTGCTTGGCCTGTAGTAGGTATCTG	4677
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAGCGAGAGTTGTTAAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATATTATAAGTTT	4678
	ATATGCTA**C**TTTTAACA	4679
	TGTTAAAA**G**TAGCATAT	4680
Triazine Resistant D1 Protein *Petunia x hybrida* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4681
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATATTATAAGTTT	4682
	ATATGCTA**C**TTTCAACA	4683
	TGTTGAAA**G**TAGCATAT	4684
Triazine Resistant D1 Protein *Magnolia pyramidata* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4685
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCAGCTACGATATTATAAGTTT	4686
	ATATGCTA**C**TTTCAACA	4687
	TGTTGAAA**G**TAGCATAT	4688
Triazine Resistant D1 Protein *Medicago sativa* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4689
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCTGCTACAATATTATAGGTTT	4690
	ATATGCTA**C**TTTCAACA	4691

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTTGAAA**G**TAGCATAT	4692
Triazine Resistant D1 Protein *Glycine max* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCAA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCTGCTTGGCCTGTAGTAGGTATTTG	4693
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCAGCTACAATATTATAGGTTT	4694
	ATATGCAA**C**TTTCAACA	4695
	TGTTGAAA**G**TTGCATAT	4696
Triazine Resistant D1 Protein *Brassica napus* Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCT**AC**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4697
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**GT**AGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4698
	ATATGCT**AC**TTTCAACA	4699
	TGTTGAAA**GT**AGCATAT	4700
Triazine Resistant D1 Protein *Oryza sativa* Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAATCTTCCAATATGCTA**C**TTTTAACAACTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGGATTTG	4701
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAGTTGTTAAAA**G**TAGCATATTGGAAGATTAATCGGCCAAAATAACCATGAGCGGCCACAATATTATAAGTTT	4702
	ATATGCTA**C**TTTTAACA	4703
	TGTTAAAA**G**TAGCATAT	4704
Triazine Resistant D1 Protein *Zea mays* Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAATCTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGGATCTG	4705
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATTAATCGACCAAAATAACCGTGAGCAGCCACAATATTATAAGTCT	4706
	ATATGCTA**C**TTTCAACA	4707
	TGTTGAAA**G**TAGCATAT	4708
Triazine Resistant D1 Protein *Arabidopsis thaliana* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATTTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4709
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAAATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4710
	ATATGCTA**C**TTTCAACA	4711
	TGTTGAAA**G**TAGCATAT	4712

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Nicotiana tabacum* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4713
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATGTTATAAGTTT	4714
	ATATGCTA**C**TTTCAACA	4715
	TGTTGAAA**G**TAGCATAT	4716
Triazine Resistant D1 Protein *Populus deltoides* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTTAACAACTCTCGCTCTTTACATTTCTTCTTAGCTGCTTGGCCTGTAGTAGGTATCTG	4717
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAGCGAGAGTTGTTAAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATATTATAAGTTT	4718
	ATATGCTA**C**TTTTAACA	4719
	TGTTAAAA**G**TAGCATAT	4720
Triazine Resistant D1 Protein *Petunia x hybrida* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4721
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATATTATAAGTTT	4722
	ATATGCTA**C**TTTCAACA	4723
	TGTTGAAA**G**TAGCATAT	4724
Triazine Resistant D1 Protein *Magnolia pyramidata* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4725
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCAGCTACGATATTATAAGTTT	4726
	ATATGCTA**C**TTTCAACA	4727
	TGTTGAAA**G**TAGCATAT	4728
Triazine Resistant D1 Protein *Medicago sativa* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4729
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCTGCTACAATATTATAGGTTT	4730
	ATATGCTA**C**TTTCAACA	4731
	TGTTGAAA**G**TAGCATAT	4732

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Glycine max* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCAA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCTGCTTGGCCTGTAGTAGGTATTTG	4733
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCAGCTACAATATTATAGGTTT	4734
	ATATGCAA**C**TTTCAACA	4735
	TGTTGAAA**G**TTGCATAT	4736
Triazine Resistant D1 Protein *Brassica napus* Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCT**AC**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4737
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4738
	ATATGCT**AC**TTTCAACA	4739
	TGTTGAAA**GT**AGCATAT	4740
Triazine Resistant D1 Protein *Oryza sativa* Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAATCTTCCAATATGCTA**C**TTTTAACAACTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGGATTTG	4741
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAGTTGTTAAAA**GT**AGCATATTGGAAGATTAATCGGCCAAAATAACCATGAGCGGCCACAATATTATAAGTTT	4742
	ATATGCTA**C**TTTTAACA	4743
	TGTTAAAA**G**TAGCATAT	4744
Triazine Resistant D1 Protein *Zea mays* Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAATCTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGGATCTG	4745
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATTAATCGACCAAAATAACCGTGAGCAGCCACAATATTATAAGTCT	4746
	ATATGCTA**C**TTTCAACA	4747
	TGTTGAAA**G**TAGCATAT	4748
Triazine Resistant D1 Protein *Arabidopsis thaliana* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATTTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4749
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAAATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4750
	ATATGCTA**C**TTTCAACA	4751
	TGTTGAAA**G**TAGCATAT	4752

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Picea abies* Ser264Thr AGT-ACT	AAACCTACAATATTGTGGCTGCTCACGGTTATTTCGGCCGATTGATCTTCCAGTATGCTA**C**TTTCAACAACTCCCGTTCTTTACATTTCTTCTTAGCTGCTTGGCCCGTAGCAGGTATCTG	4753
	CAGATACCTGCTACGGGCCAAGCAGCTAAGAAGAAATGTAAAGAACGGGAGTTGTTGAAA**G**TAGCATACTGGAAGATCAATCGGCCGAAATAACCGTGAGCAGCCACAATATTGTAGGTTT	4754
	GTATGCTA**C**TTTCAACA	4755
	TGTTGAAA**G**TAGCATAC	4756
Triazine Resistant D1 Protein *Vicia faba* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAATTCTCGCTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4757
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAGCGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATATTATAGGTTT	4758
	ATATGCTA**C**TTTCAACA	4759
	TGTTGAAA**G**TAGCATAT	4760
Triazine Resistant D1 Protein *Hordeum vulgare* Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCATGGTTATTTTGGCCGATTAATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGAATCTG	4761
	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAATAACCATGAGCAGCCACAATATTATAAGTCT	4762
	ATATGCTACTTTCAACA	4763
	TGTTGAAAGTAGCATAT	4764
Triazine Resistant D1 Protein *Triticum aestivum* Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCTGCTCATGGTTATTTTGGCCGATTAATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGAATCTG	4765
	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATTAATCGGCCAAAATAACCATGAGCAGCCACAATATTATAAGTTT	4766
	ATATGCTA**C**TTTCAACA	4767
	TGTTGAAA**G**TAGCATAT	4768
Triazine Resistant D1 Protein *Vigna unguiculata* Ser264Thr AGT-ACT	AAACTTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTAATCTTCCAATATGCAA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATTTG	4769
	CAAATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TTGCATATTGGAAGATTAATCGGCCAAAATAACCATGAGCAGCTACAATATTATAAGTTT	4770
	ATATGCAA**C**TTTCAACA	4771
	TGTTGAAA**G**TTGCATAT	4772

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Lotus japonicus* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCAA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCTTAGCTGCTTGGCCTGTTGTAGGTATCTG	4773
	CAGATACCTACAACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAACGAGAGTTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATATTATAGGTTT	4774
	ATATGCAA**C**TTTCAACA	4775
	TGTTGAAA**G**TTGCATAT	4776
Triazine Resistant D1 Protein *Sinapis alba* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4777
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4778
	ATATGCTA**C**TTTCAACA	4779
	TGTTGAAA**G**TAGCATAT	4780
Triazine Resistant D1 Protein *Pisum sativum* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAATTCTCGCTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4781
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAGCGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATATTATAGGTTT	4782
	ATATGCTA**C**TTTCAACA	4783
	TGTTGAAA**G**TAGCATAT	4784
Triazine Resistant D1 Protein *Spinacia oleracea* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGTCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCTTAGCTGCTTGGCCTGTAGTAGGTATTTG	4785
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGACCAAAATAACCATGAGCAGCTACGATATTATAAGTTT	4786
	ATATGCTA**C**TTTCAACA	4787
	TGTTGAAA**G**TAGCATAT	4788
Triazine Resistant D1 Protein *Nicotiana debneyi* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4789
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATGTTATAAGTTT	4790
	ATATGCTA**C**TTTCAACA	4791
	TGTTGAAA**G**TAGCATAT	4792

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Solanum nigrum* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**<u>C</u>**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4793
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**<u>G</u>**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATATTATAAGTTT	4794
	ATATGCTA**<u>C</u>**TTTCAACA	4795
	TGTTGAAA**<u>G</u>**TAGCATAT	4796
Triazine Resistant D1 Protein *Nicotiana plumbaginifolia* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**<u>C</u>**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4797
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**<u>G</u>**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATGTTATAAGTTT	4798
	ATATGCTA**<u>C</u>**TTTCAACA	4799
	TGTTGAAA**<u>G</u>**TAGCATAT	4800

Example 6
Engineering male- or female-sterile plants

Flower development in distantly related dicot plant species is increasingly better understood and appears to be regulated by a family of genes which encode regulatory proteins. These genes include, for example, *AGAMOUS* (*AG*), *APETALA1* (*AP1*), and *APETALA3* (*AP3*) and *PISTILLATA* (*PI*) in *Arabidopsis thaliana*, and *DEFICIENS A* (*DEFA*), *GLOBOSA* (*GLO*), *SQUAMOSA* (*SQUA*), and *PLENA* (*PLE*) in *Antirrhinum majus*. Genetic studies have shown that the *DEFA*, *GLO* and *AP3* genes are essential for petal and stamen development. Sequence analysis of these genes revealed that the gene products contain a conserved MADS box region, a DNA-binding domain. Using these clones as probes, MADS box genes have also been isolated from other species including tomato, tobacco, petunia, *Brassica napus*, and maize.

Altering the expression of these genes results in altered floral morphology. For example, mutations in *AP3* and *PI* result in male-sterile flowers because petals develop in place of stamens.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer altered floral structures in plants.

Table 14
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AP3 *Arabidopsis thaliana* Arg3Term AGA-TGA	TTGTCCTCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCG**T**GAGGGAAGATCCAGATCAAGAGGATAGAGAACCAGACAAACAGACAAGTGACGTATTCAA	4801
	TTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTCTTGATCTGGATCTTCCCTC**A**CGCCATATTCTTCTCTCTTTGTTTAATCTTTTTGTTGAAGAGATTTGGTGGAGAGGACAA	4802
	ATATGGCG**T**GAGGGAAG	4803
	CTTCCCTC**A**CGCCATAT	4804
Male-sterile AP3 *Arabidopsis thaliana* Lys5Term AAG-TAG	TCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAGGG**T**AGATCCAGATCAAGAGGATAGAGAACCAGACAAACAGACAAGTGACGTATTCAAAGAGAA	4805
	TTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTCTTGATCTGGATCT**A**CCCTCTCGCCATATTCTTCTCTCTTTGTTTAATCTTTTTGTTGAAGAGATTTGGTGGAGA	4806
	CGAGAGGG**T**AGATCCAG	4807

	CTGGATCT**A**CCCTCTCG	4808
Male-sterile AP3 *Arabidopsis thaliana* Gln7Term CAG-TAG	CCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGG CGAGAGGGAAGATC**T**AGATCAAGAGGATAGAGAACCAGACAAACA GACAAGTGACGTATTCAAAGAGAAGGAATG	4809
	CATTCCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCT ATCCTCTTGATCT**A**GATCTTCCCTCTCGCCATATTCTTCTCTCTTTG TTTAATCTTTTTGTTGAAGAGATTTGG	4810
	GGAAGATC**T**AGATCAAG	4811
	CTTGATCT**A**GATCTTCC	4812
Male-sterile AP3 *Arabidopsis thaliana* Lys9Term AAG-TAG	CTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAG GGAAGATCCAGATC**T**AGAGGATAGAGAACCAGACAAACAGACAAG TGACGTATTCAAAGAGAAGGAATGGTTTAT	4813
	ATAAACCATTCCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGG TTCTCTATCCTCT**A**GATCTGGATCTTCCCTCTCGCCATATTCTTCTC TCTTTGTTTAATCTTTTTGTTGAAGAG	4814
	TCCAGATC**T**AGAGGATA	4815
	TATCCTCT**A**GATCTGGA	4816
Male-sterile AP3 *Brassica oleracea* Lys23Term AAG-TAG	AGAGGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGA CAAGTGACGTATTCT**T**AGAGAAGAAATGGTTTGTTCAAGAAAGCTC ACGAGCTTACAGTTTTATGTGATGCTAGGG	4817
	CCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTTGAACAA ACCATTTCTTCTCT**A**AGAATACGTCACTTGTCGGTTGGTCTGGTTC TCTATCCTCTTGATCTGGATCTTCCCTCT	4818
	CGTATTCT**T**AGAGAAGA	4819
	TCTTCTCT**A**AGAATACG	4820
Male-sterile AP3 *Brassica oleracea* Arg24Term AGA-TGA	GGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAA GTGACGTATTCTAAG**T**GAAGAAATGGTTTGTTCAAGAAAGCTCACG AGCTTACAGTTTTATGTGATGCTAGGGTTT	4821
	AAACCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTTGAA CAAACCATTTCTTC**A**CTTAGAATACGTCACTTGTCGGTTGGTCTGG TTCTCTATCCTCTTGATCTGGATCTTCCC	4822
	ATTCTAAG**T**GAAGAAAT	4823
	ATTTCTTC**A**CTTAGAAT	4824
Male-sterile AP3 *Brassica oleracea* Arg25Term AGA-TGA	AAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAAGTG ACGTATTCTAAGAGA**T**GAAATGGTTTGTTCAAGAAAGCTCACGAGC TTACAGTTTTATGTGATGCTAGGGTTTCGA	4825
	TCGAAACCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTT GAACAAACCATTTC**A**TCTCTTAGAATACGTCACTTGTCGGTTGGTC TGGTTCTCTATCCTCTTGATCTGGATCTT	4826
	CTAAGAGA**T**GAAATGGT	4827
	ACCATTTC**A**TCTCTTAG	4828

Male-sterile AP3 *Brassica oleracea* Leu28Term TTG-TAG	TCAAGAGGATAGAGAACCAGACCAACCGACAAGTGACGTATTCTAAGAGAAGAAATGGTT**A**GTTCAAGAAAGCTCACGAGCTTACAGTTTTATGTGATGCTAGGGTTTCGATTATCATGTT	4829
	AACATGATAATCGAAACCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTTGAAC**T**AACCATTTCTTCTCTTAGAATACGTCACTTGTCGGTTGGTCTGGTTCTCTATCCTCTTGA	4830
	AAATGGTT**A**GTTCAAGA	4831
	TCTTGAAC**T**AACCATTT	4832
Male-sterile AP3 *Brassica napus* Tyr21Term TAC-TAG	GGCTCGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTCACCTA**G**TCCAAGAGAAGAAATGGTTTGTTCAAGAAAGCACACGAGCTCTCTGTTCTCTGTGATGCT	4833
	AGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAAACCATTTCTTCTCTTGGA**C**TAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAATCTGGATCTTCCCTCGAGCC	4834
	GTCACCTA**G**TCCAAGAG	4835
	CTCTTGGA**C**TAGGTGAC	4836
Male-sterile AP3 *Brassica napus* Lys23Term AAG-TAG	CGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTCACCTACTCC**T**AGAGAAGAAATGGTTTGTTCAAGAAAGCACACGAGCTCTCTGTTCTCTGTGATGCTAAAG	4837
	CTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAAACCATTTCTTCTCT**A**GGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAATCTGGATCTTCCCTCG	4838
	CCTACTCC**T**AGAGAAGA	4839
	TCTTCTCT**A**GGAGTAGG	4840
Male-sterile AP3 *Brassica napus* Arg24Term AGA-TGA	GGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTCACCTACTCCAAG**T**GAAGAAATGGTTTGTTCAAGAAAGCACACGAGCTCTCTGTTCTCTGTGATGCTAAAGTTT	4841
	AAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAAACCATTTCTTC**A**CTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAATCTGGATCTTCCC	4842
	ACTCCAAG**T**GAAGAAAT	4843
	ATTTCTTC**A**CTTGGAGT	4844
Male-sterile AP3 *Brassica napus* Arg25Term AGA-TGA	AAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTCACCTACTCCAAGAGA**T**GAAATGGTTTGTTCAAGAAAGCACACGAGCTCTCTGTTCTCTGTGATGCTAAAGTTTCCA	4845
	TGGAAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAAACCATTTC**A**TCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAATCTGGATCTT	4846
	CCAAGAGA**T**GAAATGGT	4847
	ACCATTTC**A**TCTCTTGG	4848

Male-sterile DEFA *Antirrhinum majus* Arg3Term CGA-TGA	GGAGAGAAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGT AGTGGTTCGATGGCT**T**GAGGGAAGATCCAGATTAAGAGGATAGAG AACCAAACAAACAGGCAGGTCACCTACTCCA	4849
	TGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAAT CTGGATCTTCCCTC**A**AGCCATCGAACCACTACCACTACTGCTCTTG TTTTCTTCTTCCAGCTTTCCTTTCTCTCC	4850
	CGATGGCT**T**GAGGGAAG	4851
	CTTCCCTC**A**AGCCATCG	4852
Male-sterile DEFA *Antirrhinum majus* Lys5Term AAG-TAG	AAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGT TCGATGGCTCGAGGG**T**AGATCCAGATTAAGAGGATAGAGAACCAA ACAAACAGGCAGGTCACCTACTCCAAGAGAA	4853
	TTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCT CTTAATCTGGATCT**A**CCCTCGAGCCATCGAACCACTACCACTACTG CTCTTGTTTTCTTCTTCCAGCTTTCCTTT	4854
	CTCGAGGG**T**AGATCCAG	4855
	CTGGATCT**A**CCCTCGAG	4856
Male-sterile DEFA *Antirrhinum majus* Gln7Term CAG-TAG	AAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATG GCTCGAGGGAAGATC**T**AGATTAAGAGGATAGAGAACCAAACAAAC AGGCAGGTCACCTACTCCAAGAGAAGAAATG	4857
	CATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTC TATCCTCTTAATCT**A**GATCTTCCCTCGAGCCATCGAACCACTACCA CTACTGCTCTTGTTTTCTTCTTCCAGCTT	4858
	GGAAGATC**T**AGATTAAG	4859
	CTTAATCT**A**GATCTTCC	4860
Male-sterile DEFA *Antirrhinum majus* Lys9Term AAG-TAG	GAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTCGA GGGAAGATCCAGATT**T**AGAGGATAGAGAACCAAACAAACAGGCAG GTCACCTACTCCAAGAGAAGAAATGGTTTGT	4861
	ACAAACCATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTG GTTCTCTATCCTCT**A**AATCTGGATCTTCCCTCGAGCCATCGAACCA CTACCACTACTGCTCTTGTTTTCTTCTTC	4862
	TCCAGATT**T**AGAGGATA	4863
	TATCCTCT**A**AATCTGGA	4864
Male-sterile AP3 *Nicotiana tabacum* Lys5Term AAG-TAG	TCAGTAATTCTTAAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAAC TATGGCTCGTGGG**T**AGATCCAGATCAAGAGAATAGAGAACCAAAC AAACAGACAAGTCACTTATTCTAAGAGAA	4865
	TTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGGTTCTCTATTCTC TTGATCTGGATCT**A**CCCACGAGCCATAGTTTTTTTTTCTTTTTGCTC AAAGTTTGAGATCTTAAGAATTACTGA	4866
	CTCGTGGG**T**AGATCCAG	4867
	CTGGATCT**A**CCCACGAG	4868

Male-sterile AP3 *Nicotiana tabacum* Gln7Term CAG-TAG	ATTCTTAAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGC TCGTGGGAAGATC**T**AGATCAAGAGAATAGAGAACCAAACAAACAGA CAAGTCACTTATTCTAAGAGAAGAAATG	4869
	CATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGGTTCTCT ATTCTCTTGATCT**A**GATCTTCCCACGAGCCATAGTTTTTTTTTCTTT TTGCTCAAAGTTTGAGATCTTAAGAAT	4870
	GGAAGATC**T**AGATCAAG	4871
	CTTGATCT**A**GATCTTCC	4872
Male-sterile AP3 *Nicotiana tabacum* Lys9Term AAG-TAG	AAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGCTCGTG GGAAGATCCAGATC**T**AGAGAATAGAGAACCAAACAAACAGACAAGT CACTTATTCTAAGAGAAGAAATGGACTTT	4873
	AAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGG TTCTCTATTCTCT**A**GATCTGGATCTTCCCACGAGCCATAGTTTTTTT TTCTTTTTGCTCAAAGTTTGAGATCTT	4874
	TCCAGATC**T**AGAGAATA	4875
	TATTCTCT**A**GATCTGGA	4876
Male-sterile AP3 *Nicotiana tabacum* Arg10Term AGA-TGA	ATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGCTCGTGGGA AGATCCAGATCAAG**T**GAATAGAGAACCAAACAAACAGACAAGTCAC TTATTCTAAGAGAAGAAATGGACTTTTCA	4877
	TGAAAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTT TGGTTCTCTATTC**A**CTTGATCTGGATCTTCCCACGAGCCATAGTTT TTTTTTCTTTTTGCTCAAAGTTTGAGAT	4878
	AGATCAAG**T**GAATAGAG	4879
	CTCTATTC**A**CTTGATCT	4880
Male-sterile AP3 *Medicago sativa* Tyr21Term TAC-TAG	GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAA CAGACAAGTAACTTA**G**TCAAAACGAAGGGATGGTCTTTTCAAGAAG GCCAATGAGCTCACTGTTCTTTGTGATGCT	4881
	AGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGACCA TCCCTTCGTTTTGA**C**TAAGTTACTTGTCTGTTCGTTGTGTTCTCTAT TCTCTTGATCTGGATCTTTCCTCGAGCC	4882
	GTAACTTA**G**TCAAAACG	4883
	CGTTTTGA**C**TAAGTTAC	4884
Male-sterile AP3 *Medicago sativa* Ser22Term TCA-TGA	CTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACA GACAAGTAACTTACT**G**AAAACGAAGGGATGGTCTTTTCAAGAAGGC CAATGAGCTCACTGTTCTTTGTGATGCTAA	4885
	TTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGAC CATCCCTTCGTTTT**C**AGTAAGTTACTTGTCTGTTCGTTGTGTTCTCT ATTCTCTTGATCTGGATCTTTCCTCGAG	4886
	AACTTACT**G**AAAACGAA	4887
	TTCGTTTT**C**AGTAAGTT	4888

Male-sterile AP3 *Medicago sativa* Lys23Term AAA-TAA	CGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGA CAAGTAACTTACTCA**T**AACGAAGGGATGGTCTTTTCAAGAAGGCCA ATGAGCTCACTGTTCTTTGTGATGCTAAGG	4889
	CCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAG ACCATCCCTTCGTT**A**TGAGTAAGTTACTTGTCTGTTCGTTGTGTTCT CTATTCTCTTGATCTGGATCTTTCCTCG	4890
	CTTACTCA**T**AACGAAGG	4891
	CCTTCGTT**A**TGAGTAAG	4892
Male-sterile AP3 *Medicago sativa* Arg24Term CGA-TGA	GGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAA GTAACTTACTCAAAA**T**GAAGGGATGGTCTTTTCAAGAAGGCCAATG AGCTCACTGTTCTTTGTGATGCTAAGGTTT	4893
	AAACCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAA AAGACCATCCCTTC**A**TTTTGAGTAAGTTACTTGTCTGTTCGTTGTGT TCTCTATTCTCTTGATCTGGATCTTTCC	4894
	ACTCAAAA**T**GAAGGGAT	4895
	ATCCCTTC**A**TTTTGAGT	4896
Male-sterile DEF4 *Solanum tuberosum* Tyr21Term TAT-TAG	GGCTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAAT AGGCAAGTGACTTA**G**TCAAAGAGAAGAAATGGGCTATTCAAGAAG GCTAATGAACTTACAGTTCTTTGTGATGCT	4897
	AGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCA TTTCTTCTCTTTGA**C**TAAGTCACTTGCCTATTTGTTTGGTTTTCTATT TTCTTGATCTGGATCTTACCACGAGCC	4898
	GTGACTTA**G**TCAAAGAG	4899
	CTCTTTGA**C**TAAGTCAC	4900
Male-sterile DEF4 *Solanum tuberosum* Ser22Term TCA-TGA	CTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAG GCAAGTGACTTATT**G**AAAGAGAAGAAATGGGCTATTCAAGAAGGCT AATGAACTTACAGTTCTTTGTGATGCTAA	4901
	TTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCC CATTTCTTCTCTTT**C**AATAAGTCACTTGCCTATTTGTTTGGTTTTCTA TTTTCTTGATCTGGATCTTACCACGAG	4902
	GACTTATT**G**AAAGAGAA	4903
	TTCTCTTT**C**AATAAGTC	4904
Male-sterile DEF4 *Solanum tuberosum* Lys23Term AAG-TAG	CGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGC AAGTGACTTATTCA**T**AGAGAAGAAATGGGCTATTCAAGAAGGCTAA TGAACTTACAGTTCTTTGTGATGCTAAAG	4905
	CTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGC CCATTTCTTCTCT**A**TGAATAAGTCACTTGCCTATTTGTTTGGTTTTC TATTTTCTTGATCTGGATCTTACCACG	4906
	CTTATTCA**T**AGAGAAGA	4907
	TCTTCTCT**A**TGAATAAG	4908

Male-sterile DEF4 *Solanum tuberosum* Arg24Term AGA-TGA	GGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAAGTGACTTATTCAAAG**T**GAAGAAATGGGCTATTCAAGAAGGCTAATGAACTTACAGTTCTTTGTGATGCTAAAGTTT	4909
	AAACTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCATTTCTTC**A**CTTTGAATAAGTCACTTGCCTATTTGTTTGGTTTTCTATTTTCTTGATCTGGATCTTACC	4910
	ATTCAAAG**T**GAAGAAAT	4911
	ATTTCTTC**A**CTTTGAAT	4912
Male-sterile AP3 *Lycopersicon esculentum* Gly27Term GGA-TGA	GCTAATGAACTTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTACT**T**GAAAACTTCATGAGTTTATAAGTCCCTCTATCACGACCAAACAATTGTTCGATCTGTACC	4913
	GGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAACTCATGAAGTTTTC**A**AGTACTAGAAATCATAACAATTGAAACTTTAGCATCACAAAGAACAGTAAGTTCATTAGC	4914
	CTAGTACT**T**GAAAACTT	4915
	AAGTTTTC**A**AGTACTAG	4916
Male-sterile AP3 *Lycopersicon esculentum* Lys28Term AAA-TAA	AATGAACTTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTACTGGA**T**AACTTCATGAGTTTATAAGTCCCTCTATCACGACCAAACAATTGTTCGATCTGTACCAGA	4917
	TCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAACTCATGAAGTT**A**TCCAGTACTAGAAATCATAACAATTGAAACTTTAGCATCACAAAGAACAGTAAGTTCATT	4918
	GTACTGGA**T**AACTTCAT	4919
	ATGAAGTT**A**TCCAGTAC	4920
Male-sterile AP3 *Lycopersicon esculentum* Glu31Term GAG-TAG	ACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTACTGGAAAACTTCAT**T**AGTTTATAAGTCCCTCTATCACGACCAAACAATTGTTCGATCTGTACCAGAAGACTATTG	4921
	CAATAGTCTTCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAACT**A**ATGAAGTTTTCCAGTACTAGAAATCATAACAATTGAAACTTTAGCATCACAAAGAACAGT	4922
	AACTTCAT**T**AGTTTATA	4923
	TATAAACT**A**ATGAAGTT	4924
Male-sterile AP3 *Lycopersicon esculentum* Lys40Term AAA-TAA	ATTGTTATGATTTCTAGTACTGGAAAACTTCATGAGTTTATAAGTCCCTCTATCACGACC**T**AACAATTGTTCGATCTGTACCAGAAGACTATTGGAGTTGATATTTGGACTACTCACTATG	4925
	CATAGTGAGTAGTCCAAATATCAACTCCAATAGTCTTCTGGTACAGATCGAACAATTGTT**A**GGTCGTGATAGAGGGACTTATAAACTCATGAAGTTTTCCAGTACTAGAAATCATAACAAT	4926
	TCACGACC**T**AACAATTG	4927
	CAATTGTT**A**GGTCGTGA	4928

Male-sterile AP3 *Triticum aestivum* Tyr21Term TAC-TAG	GGGGCGGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCTA**G**TCCAAGCGCCGGTCGGGGATCATGAAGAAGGCGCGGGAGCTCACCGTGCTCTGCGACGCC	4929
	GGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATGATCCCCGACCGGCGCTTGGA**C**TAGGTCACCTGCCTGTTGGTGGCGTTCTCGATCCGCTTTATCTCAATCTTCCCCCGCCCC	4930
	GTGACCTA**G**TCCAAGCG	4931
	CGCTTGGA**C**TAGGTCAC	4932
Male-sterile AP3 *Triticum aestivum* Lys23Term AAG-TAG	CGGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCC**T**AGCGCCGGTCGGGGATCATGAAGAAGGCGCGGGAGCTCACCGTGCTCTGCGACGCCCAGG	4933
	CCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATGATCCCCGACCGGCGCT**A**GGAGTAGGTCACCTGCCTGTTGGTGGCGTTCTCGATCCGCTTTATCTCAATCTTCCCCCG	4934
	CCTACTCC**T**AGCGCCGG	4935
	CCGGCGCT**A**GGAGTAGG	4936
Male-sterile AP3 *Triticum aestivum* Ser26Term TCG-TAG	TTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCCAAGCGCCGGT**A**GGGGATCATGAAGAAGGCGCGGGAGCTCACCGTGCTCTGCGACGCCCAGGTCGCCATCAT	4937
	ATGATGGCGACCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATGATCCCC**T**ACCGGCGCTTGGAGTAGGTCACCTGCCTGTTGGTGGCGTTCTCGATCCGCTTTATCTCAA	4938
	GCGCCGGT**A**GGGGATCA	4939
	TGATCCCC**T**ACCGGCGC	4940
Male-sterile AP3 *Triticum aestivum* Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCCAAGCGCCGGTCGGGGATCATG**T**AGAAGGCGCGGGAGCTCACCGTGCTCTGCGACGCCCAGGTCGCCATCATCATGTTCTCCT	4941
	AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCT**A**CATGATCCCCGACCGGCGCTTGGAGTAGGTCACCTGCCTGTTGGTGGCGTTCTCGATCCG	4942
	GGATCATG**T**AGAAGGCG	4943
	CGCCTTCT**A**CATGATCC	4944
Male-sterile Silky1 *Zea mays* Tyr21Term TAC-TAG	GGGGCGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCGCCAGGTGACCTA**G**TCCAAGCGCCGGACGGGGATCATGAAGAAGGCACGCGAGCTCACCGTGCTCTGCGACGCC	4945
	GGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATGATCCCCGTCCGGCGCTTGGA**C**TAGGTCACCTGGCGGTTGGTGGCGTTCTCGATCCGCTTGATCTCGATCTTGCCGCGCCCC	4946
	GTGACCTA**G**TCCAAGCG	4947
	CGCTTGGA**C**TAGGTCAC	4948

Male-sterile Silky1 *Zea mays* Lys23Term AAG-TAG	CGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCG CCAGGTGACCTACTCC**T**AGCGCCGGACGGGGATCATGAAGAAGG CACGCGAGCTCACCGTGCTCTGCGACGCCCAGG	4949
	CCTGGGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATG ATCCCCGTCCGGCGCT**A**GGAGTAGGTCACCTGGCGGTTGGTGGC GTTCTCGATCCGCTTGATCTCGATCTTGCCGCG	4950
	CCTACTCC**T**AGCGCCGG	4951
	CCGGCGCT**A**GGAGTAGG	4952
Male-sterile Silky1 *Zea mays* Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCG CCGGACGGGGATCATG**T**AGAAGGCACGCGAGCTCACCGTGCTCT GCGACGCCCAGGTCGCCATCATCATGTTCTCCT	4953
	AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG AGCTCGCGTGCCTTCT**A**CATGATCCCCGTCCGGCGCTTGGAGTAG GTCACCTGGCGGTTGGTGGCGTTCTCGATCCG	4954
	GGATCATG**T**AGAAGGCA	4955
	TGCCTTCT**A**CATGATCC	4956
Male-sterile Silky1 *Zea mays* Lys31Term AAG-TAG	ATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCGCCG GACGGGGATCATGAAG**T**AGGCACGCGAGCTCACCGTGCTCTGCG ACGCCCAGGTCGCCATCATCATGTTCTCCTCCA	4957
	TGGAGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACG GTGAGCTCGCGTGCCT**A**CTTCATGATCCCCGTCCGGCGCTTGGA GTAGGTCACCTGGCGGTTGGTGGCGTTCTCGAT	4958
	TCATGAAG**T**AGGCACGC	4959
	GCGTGCCT**A**CTTCATGA	4960
Male-sterile AP3 *Oryza sativa* Lys5Term AAG-TAG	GCTAGCTGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGC GGCCATGGGGAGGGGC**T**AGATCGAGATCAAGCGGATCGAGAACG CGACCAACAGGCAGGTGACCTACTCGAAGCGCC	4961
	GGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCGCGTTCTCGATCC GCTTGATCTCGATCT**A**GCCCCTCCCCATGGCCGCCCCCTGCAGC AGCTATCTCTCTCGCCGGACAATGCAGCTAGC	4962
	GGAGGGGC**T**AGATCGAG	4963
	CTCGATCT**A**GCCCCTCC	4964
Male-sterile AP3 *Oryza sativa* Glu7Term GAG-TAG	TGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCAT GGGGAGGGGCAAGATC**T**AGATCAAGCGGATCGAGAACGCGACCA ACAGGCAGGTGACCTACTCGAAGCGCCGCACGG	4965
	CCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCGCGTTCT CGATCCGCTTGATCT**A**GATCTTGCCCCTCCCCATGGCCGCCCCCT GCAGCAGCTATCTCTCTCGCCGGACAATGCA	4966
	GCAAGATC**T**AGATCAAG	4967
	CTTGATCT**A**GATCTTGC	4968

Male-sterile AP3 *Oryza sativa* Lys9Term AAG-TAG	GTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGA GGGGCAAGATCGAGATC**T**AGCGGATCGAGAACGCGACCAACAGG CAGGTGACCTACTCGAAGCGCCGCACGGGGATCA	4969
	TGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTC GCGTTCTCGATCCGCT**A**GATCTCGATCTTGCCCCTCCCCATGGCC GCCCCCTGCAGCAGCTATCTCTCTCGCCGGAC	4970
	TCGAGATC**T**AGCGGATC	4971
	GATCCGCT**A**GATCTCGA	4972
Male-sterile AP3 *Oryza sativa* Glu12Term GAG-TAG	GAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCAAGA TCGAGATCAAGCGGATC**T**AGAACGCGACCAACAGGCAGGTGACCT ACTCGAAGCGCCGCACGGGGATCATGAAGAAGG	4973
	CCTTCTTCATGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCC TGTTGGTCGCGTTCT**A**GATCCGCTTGATCTCGATCTTGCCCCTCC CCATGGCCGCCCCCTGCAGCAGCTATCTCTC	4974
	AGCGGATC**T**AGAACGCG	4975
	CGCGTTCT**A**GATCCGCT	4976

Table 15
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Arabidopsis thaliana* Tyr35Term TAC-TAG	TCTGTACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCA GCAATCACGGCGTA**G**CAATCGGAGCTAGGAGGAGATTCCTCTCC CTTGAGGAAATCTGGGAGAGGAAAGATCGAA	4977
	TTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCCT CCTAGCTCCGATTG**C**TACGCCGTGATTGCTGCTCCAAAGCCAAAA ACGTTTAGGGCAAAATTTGATTAGTACAGA	4978
	ACGGCGTA**G**CAATCGGA	4979
	TCCGATTG**C**TACGCCGT	4980
Male-sterile AG *Arabidopsis thaliana* Gln36Term CAA-TAA	CTGTACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAG CAATCACGGCGTAC**T**AATCGGAGCTAGGAGGAGATTCCTCTCCCT TGAGGAAATCTGGGAGAGGAAAGATCGAAA	4981
	TTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCC TCCTAGCTCCGATT**A**GTACGCCGTGATTGCTGCTCCAAAGCCAAA AACGTTTAGGGCAAAATTTGATTAGTACAG	4982
	CGGCGTAC**T**AATCGGAG	4983
	CTCCGATT**A**GTACGCCG	4984

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Arabidopsis thaliana* Ser37Term TCG-TAG	ACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAGCAATCACGGCGTACCAAT**A**GGAGCTAGGAGGAGATTCCTCTCCCTTGAGGAAATCTGGGAGAGGAAAGATCGAAATCAA	4985
	TTGATTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCCTCCTAGCTCC**T**ATTGGTACGCCGTGATTGCTGCTCCAAAGCCAAAAACGTTTAGGGCAAAATTTGATTAGT	4986
	GTACCAAT**A**GGAGCTAG	4987
	CTAGCTCC**T**ATTGGTAC	4988
Male-sterile AG *Arabidopsis thaliana* Glu38Term GAG-TAG	TAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAGCAATCACGGCGTACCAATCG**T**AGCTAGGAGGAGATTCCTCTCCCTTGAGGAAATCTGGGAGAGGAAAGATCGAAATCAAAC	4989
	GTTTGATTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCCTCCTAGCT**A**CGATTGGTACGCCGTGATTGCTGCTCCAAAGCCAAAAACGTTTAGGGCAAAATTTGATTA	4990
	ACCAATCG**T**AGCTAGGA	4991
	TCCTAGCT**A**CGATTGGT	4992
Male-sterile AG *Brassica napus* Glu3Term GAA-TAA	CTCTCCCACTTCTTTTCGGTGGTTTATTCATTTGGTGACGATATCACAGAAGCAATGGAT**T**AAGGTGGGAGTAGTCACGATGCAGAGAGTAGCAAGAAGATAGGTAGAGGGAAGATAGAGA	4993
	TCTCTATCTTCCCTCTACCTATCTTCTTGCTACTCTCTGCATCGTGACTACTCCCACCTT**A**ATCCATTGCTTCTGTGATATCGTCACCAAATGAATAAACCACCGAAAAGAAGTGGGAGAG	4994
	CAATGGAT**T**AAGGTGGG	4995
	CCCACCTT**A**ATCCATTG	4996
Male-sterile AG *Brassica napus* Glu11Term GAG-TAG	TATTCATTTGGTGACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGATGCA**T**AGAGTAGCAAGAAGATAGGTAGAGGGAAGATAGAGATAAAGAGGATAGAGAACACAACAA	4997
	TTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCTCTACCTATCTTCTTGCTACTCT**A**TGCATCGTGACTACTCCCACCTTCATCCATTGCTTCTGTGATATCGTCACCAAATGAATA	4998
	ACGATGCA**T**AGAGTAGC	4999
	GCTACTCT**A**TGCATCGT	5000
Male-sterile AG *Brassica napus* Lys14Term AAG-TAG	GGTGACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGATGCAGAGAGTAGC**T**AGAAGATAGGTAGAGGGAAGATAGAGATAAAGAGGATAGAGAACACAACAAATCGTCAAG	5001
	CTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCTCTACCTATCTTCT**A**GCTACTCTCTGCATCGTGACTACTCCCACCTTCATCCATTGCTTCTGTGATATCGTCACC	5002
	AGAGTAGC**T**AGAAGATA	5003
	TATCTTCT**A**GCTACTCT	5004

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Brassica napus* Lys15Term AAG-TAG	GACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGAT GCAGAGAGTAGCAAG**T**AGATAGGTAGAGGGAAGATAGAGATAAAG AGGATAGAGAACACAACAAATCGTCAAGTAA	5005
	TTACTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTC CCTCTACCTATCT**A**CTTGCTACTCTCTGCATCGTGACTACTCCCAC CTTCATCCATTGCTTCTGTGATATCGTC	5006
	GTAGCAAG**T**AGATAGGT	5007
	ACCTATCT**A**CTTGCTAC	5008
Male-sterile AG *Lycopersicon esculentum* Glu4Term CAA-TAA	CAACCAAAAAACTTAAAAATCTTCTCTTTCCTTTCCTTACAAGGTGA AGTAATGGACTTC**T**AAAGTGATCTAACCAGAGAGATCTCACCACAA AGGAAACTAGGAAGGGGGAAAATTGAGA	5009
	TCTCAATTTTCCCCCTTCCTAGTTTCCTTTGTGGTGAGATCTCTCT GGTTAGATCACTTT**A**GAAGTCCATTACTTCACCTTGTAAGGAAAGG AAAGAGAAGATTTTTAAGTTTTTTGGTTG	5010
	TGGACTTC**T**AAAGTGAT	5011
	ATCACTTT**A**GAAGTCCA	5012
Male-sterile AG *Lycopersicon esculentum* Arg9Term AGA-TGA	AAAATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCC AAAGTGATCTAACC**T**GAGAGATCTCACCACAAAGGAAACTAGGAA GGGGGAAAATTGAGATCAAAAGGATCGAAA	5013
	TTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAGTTTCCTTTGT GGTGAGATCTCTC**A**GGTTAGATCACTTTGGAAGTCCATTACTTCAC CTTGTAAGGAAAGGAAAGAGAAGATTTT	5014
	ATCTAACC**T**GAGAGATC	5015
	GATCTCTC**A**GGTTAGAT	5016
Male-sterile AG *Lycopersicon esculentum* Glu10Term GAG-TAG	ATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAA GTGATCTAACCAGA**T**AGATCTCACCACAAAGGAAACTAGGAAGGG GGAAAATTGAGATCAAAAGGATCGAAAACA	5017
	TGTTTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAGTTTCCTT TGTGGTGAGATCT**A**TCTGGTTAGATCACTTTGGAAGTCCATTACTT CACCTTGTAAGGAAAGGAAAGAGAAGAT	5018
	TAACCAGA**T**AGATCTCA	5019
	TGAGATCT**A**TCTGGTTA	5020
Male-sterile AG *Lycopersicon esculentum* Ser12Term TCA-TGA	CTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCT AACCAGAGAGATCT**G**ACCACAAAGGAAACTAGGAAGGGGGAAAAT TGAGATCAAAAGGATCGAAAACACGACGAA	5021
	TTCGTCGTGTTTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTA GTTTCCTTTGTGGT**C**AGATCTCTCTGGTTAGATCACTTTGGAAGTC CATTACTTCACCTTGTAAGGAAAGGAAAG	5022
	AGAGATCT**G**ACCACAAA	5023

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTTGTGGT**C**AGATCTCT	5024
Male-sterile NAG1 *Nicotiana tabacum* Gln4Term CAA-TAA	GTACTCTCTATTTTCATCTTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTC**T**AAAGTGATCTAACAAGAGAGATCTCTCCACAAAGGAAACTGGGAAGAGGAAAGATTGAGA	5025
	TCTCAATCTTTCCTCTTCCCAGTTTCCTTTGTGGAGAGATCTCTCTTGTTAGATCACTTT**A**GAAGTCCATACTTTCACCTGGTAAGGAAAGAAAGGGTTGGAAGATGAAAATAGAGAGTAC	5026
	TGGACTTC**T**AAAGTGAT	5027
	ATCACTTT**A**GAAGTCCA	5028
Male-sterile NAG1 *Nicotiana tabacum* Arg9Term AGA-TGA	ATCTTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACA**T**GAGAGATCTCTCCACAAAGGAAACTGGGAAGAGGAAAGATTGAGATCAAACGGATCGAAA	5029
	TTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCCAGTTTCCTTTGTGGAGAGATCTCTC**A**TGTTAGATCACTTTGGAAGTCCATACTTTCACCTGGTAAGGAAAGAAAGGGTTGGAAGAT	5030
	ATCTAACA**T**GAGAGATC	5031
	GATCTCTC**A**TGTTAGAT	5032
Male-sterile NAG1 *Nicotiana tabacum* Glu10Term GAG-TAG	TTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACAAGA**T**AGATCTCTCCACAAAGGAAACTGGGAAGAGGAAAGATTGAGATCAAACGGATCGAAAACA	5033
	TGTTTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCCAGTTTCCTTTGTGGAGAGATCT**A**TCTTGTTAGATCACTTTGGAAGTCCATACTTTCACCTGGTAAGGAAAGAAAGGGTTGGAA	5034
	TAACAAGA**T**AGATCTCT	5035
	AGAGATCT**A**TCTTGTTA	5036
Male-sterile NAG1 *Nicotiana tabacum* Gln14Term CAA-TAA	CTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACAAGAGAGATCTCTCCA**T**AAAGGAAACTGGGAAGAGGAAAGATTGAGATCAAACGGATCGAAAACACAACGAATCGTC	5037
	GACGATTCGTTGTGTTTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCCAGTTTCCTTT**A**TGGAGAGATCTCTCTTGTTAGATCACTTTGGAAGTCCATACTTTCACCTGGTAAGGAAAG	5038
	TCTCTCCA**T**AAAGGAAA	5039
	TTTCCTTT**A**TGGAGAGA	5040
Male-sterile AG *Rosa hybrida* Gly22Term GGA-TGA	GCCTATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAGG**T**GAAAGATCGAGATCAAGCGGATCGAAAACACCACCAATCGTCAAGTCACCTTCTGCAAAA	5041
	TTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTTCGATCCGCTTGATCTCGATCTTTC**A**CCTTCCCAATCTTCTTTGGGCATCAGCGTCCAGGACCGTGTTGGGTTTGTTTTCATAGGC	5042
	TGGGAAGG**T**GAAAGATC	5043
	GATCTTTC**A**CCTTCCCA	5044

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Rosa hybrida* Lys23Term AAG-TAG	TATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAGGGGA**T**AGATCGAGATCAAGCGGATCGAAAACACCACCAATCGTCAAGTCACCTTCTGCAAAAGGC	5045
	GCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTTCGATCCGCTTGATCTCGATCT**A**TCCCCTTCCCAATCTTCTTTGGGCATCAGCGTCCAGGACCGTGTTGGGTTTGTTTTCATA	5046
	GAAGGGGA**T**AGATCGAG	5047
	CTCGATCT**A**TCCCCTTC	5048
Male-sterile AG *Rosa hybrida* Glu25Term GAG-TAG	AACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAGGGGAAAGATC**T**AGATCAAGCGGATCGAAAACACCACCAATCGTCAAGTCACCTTCTGCAAAAGGCGCAATG	5049
	CATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTTCGATCCGCTTGATCT**A**GATCTTTCCCCTTCCCAATCTTCTTTGGGCATCAGCGTCCAGGACCGTGTTGGGTTTGTT	5050
	GAAAGATC**T**AGATCAAG	5051
	CTTGATCT**A**GATCTTTC	5052
Male-sterile AG *Rosa hybrida* Lys27 AAG-TAG	CCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAGGGGAAAGATCGAGATC**T**AGCGGATCGAAAACACCACCAATCGTCAAGTCACCTTCTGCAAAAGGCGCAATGGTTTGC	5053
	GCAAACCATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTTCGATCCGCT**A**GATCTCGATCTTTCCCCTTCCCAATCTTCTTTGGGCATCAGCGTCCAGGACCGTGTTGGG	5054
	TCGAGATC**T**AGCGGATC	5055
	GATCCGCT**A**GATCTCGA	5056
Male-sterile far *Antirrhinum majus* Gln7Term CAA-TAA	CAATTGCCTGTTTTTATTTTTTTTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAGCGATT**T**AATCGACCGAGGTATCGCCCGAGAGGAAAATCGGGAGAGGAAAGATCGAGATCAAACGGA	5057
	TCCGTTTGATCTCGATCTTTCCTCTCCCGATTTTCCTCTCGGGCGATACCTCGGTCGATT**A**ATCGCTTAGAGACGCCATTTCTACTTAGTCAAAAAGAAAAAAAAATAAAAACAGGCAATTG	5058
	TAAGCGATT**T**AATCGACC	5059
	GGTCGATT**A**ATCGCTTA	5060
Male-sterile far *Antirrhinum majus* Glu10Term GAG-TAG	GTTTTTATTTTTTTTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGACC**T**AGGTATCGCCCGAGAGGAAAATCGGGAGAGGAAAGATCGAGATCAAACGGATCGAAAACA	5061
	TGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTCCCGATTTTCCTCTCGGGCGATACCT**A**GGTCGATTGATCGCTTAGAGACGCCATTTCTACTTAGTCAAAAAGAAAAAAAATAAAAAC	5062
	AATCGACC**T**AGGTATCG	5063
	CGATACCT**A**GGTCGATT	5064

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile far *Antirrhinum majus* Glu14Term GAG-TAG	TTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGACCGAGGTATCGCCC**T**AGAGGAAAATCGGGAGAGGAAAGATCGAGATCAAACGGATCGAAAACAAAACAAATCAAC	5065
	GTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTCCCGATTTTCCTCT**A**GGGCGATACCTCGGTCGATTGATCGCTTAGAGACGCCATTTCTACTTAGTCAAAAAGAAA	5066
	TATCGCCC**T**AGAGGAAA	5067
	TTTCCTCT**A**GGGCGATA	5068
Male-sterile far *Antirrhinum majus* Lys16Term AAA-TAA	TTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGACCGAGGTATCGCCCGAGAGG**T**AAATCGGGAGAGGAAAGATCGAGATCAAACGGATCGAAAACAAAACAAATCAACAGGTTA	5069
	TAACCTGTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTCCCGATTT**A**CCTCTCGGGCGATACCTCGGTCGATTGATCGCTTAGAGACGCCATTTCTACTTAGTCAAA	5070
	CCGAGAGG**T**AAATCGGG	5071
	CCCGATTT**A**CCTCTCGG	5072
Male-sterile AG *Cucumis sativus* Leu21Term TTG-TAG	TGTCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAGGGTAAGT**A**GCAAATAAAGGGGATGTTCCAGAATCAAGAAGAGAAGATGTCAGACTCGCCTCAGAGGAA	5073
	TTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAACATCCCCTTTATTTGC**T**ACTTACCCTTTCCTTCTTCCTTAATCATTCTTGTGAGTGGTGACTGATAATGCTTGGACA	5074
	GGGTAAGT**A**GCAAATAA	5075
	TTATTTGC**T**ACTTACCC	5076
Male-sterile AG *Cucumis sativus* Gln22Term CAA-TAA	TCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAGGGTAAGTTG**T**AAATAAAGGGGATGTTCCAGAATCAAGAAGAGAAGATGTCAGACTCGCCTCAGAGGAAGA	5077
	TCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAACATCCCCTTTATTT**A**CAACTTACCCTTTCCTTCTTCCTTAATCATTCTTGTGAGTGGTGACTGATAATGCTTGGA	5078
	GTAAGTTG**T**AAATAAAG	5079
	CTTTATTT**A**CAACTTAC	5080
Male-sterile AG *Cucumis sativus* Lys24Term AAG-TAG	CATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAGGGTAAGTTGCAAATA**T**AGGGGATGTTCCAGAATCAAGAAGAGAAGATGTCAGACTCGCCTCAGAGGAAGATGGGAA	5081
	TTCCCATCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAACATCCCCT**A**TATTTGCAACTTACCCTTTCCTTCTTCCTTAATCATTCTTGTGAGTGGTGACTGATAATG	5082
	TGCAAATA**T**AGGGGATG	5083
	CATCCCCT**A**TATTTGCA	5084

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Cucumis sativus* Gln28Term CAG-TAG	CCACTCACAAGAATGATTAAGGAAGAAGGAAAGGGTAAGTTGCAA ATAAAGGGGATGTTC**T**AGAATCAAGAAGAGAAGATGTCAGACTCG CCTCAGAGGAAGATGGGAAGAGGAAAGATTG	5085
	CAATCTTTCCTCTTCCCATCTTCCTCTGAGGCGAGTCTGACATCTT CTCTTCTTGATTCT**A**GAACATCCCCTTTATTTGCAACTTACCCTTTC CTTCTTCCTTAATCATTCTTGTGAGTGG	5086
	GGATGTTC**T**AGAATCAA	5087
	TTGATTCT**A**GAACATCC	5088
Male-sterile AG *Zea mays* Cys10Term TGC-TGA	CCACCACCACCACCACCACCACCACCACACCATGCTCAACATGAT GACTGATCTGAGCTG**A**GGGCCGTCGTCCAAGGTCAAGGAGCAGG TGGCGGCGGCGCCGACGGGCTCCGGCGACAGG	5089
	CCTGTCGCCGGAGCCCGTCGGCGCCGCCGCCACCTGCTCCTTG ACCTTGGACGACGGCCC**T**CAGCTCAGATCAGTCATCATGTTGAGC ATGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG	5090
	CTGAGCTG**A**GGGCCGTC	5091
	GACGGCCC**T**CAGCTCAG	5092
Male-sterile AG *Zea mays* Ser13Term TCG-TAG	ACCACCACCACCACCACCACACCATGCTCAACATGATGACTGATC TGAGCTGCGGGCCGT**A**GTCCAAGGTCAAGGAGCAGGTGGCGGC GGCGCCGACGGGCTCCGGCGACAGGCAGGGGCA	5093
	TGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCCGCCGCCACCT GCTCCTTGACCTTGGAC**T**ACGGCCCGCAGCTCAGATCAGTCATCA TGTTGAGCATGGTGTGGTGGTGGTGGTGGTGGT	5094
	CGGGCCGT**A**GTCCAAGG	5095
	CCTTGGAC**T**ACGGCCCG	5096
Male-sterile AG *Zea mays* Lys15Term AAG-TAG	CACCACCACCACCACACCATGCTCAACATGATGACTGATCTGAGC TGCGGGCCGTCGTCC**T**AGGTCAAGGAGCAGGTGGCGGCGGCGC CGACGGGCTCCGGCGACAGGCAGGGGCAGGGGA	5097
	TCCCCTGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCCGCCGC CACCTGCTCCTTGACCT**A**GGACGACGGCCCGCAGCTCAGATCAG TCATCATGTTGAGCATGGTGTGGTGGTGGTGGTG	5098
	CGTCGTCC**T**AGGTCAAG	5099
	CTTGACCT**A**GGACGACG	5100
Male-sterile AG *Zea mays* Lys17Term AAG-TAG	CACCACCACACCATGCTCAACATGATGACTGATCTGAGCTGCGGG CCGTCGTCCAAGGTC**T**AGGAGCAGGTGGCGGCGGCGCCGACGG GCTCCGGCGACAGGCAGGGGCAGGGGAGAGGCA	5101
	TGCCTCTCCCCTGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGC CGCCGCCACCTGCTCCT**A**GACCTTGGACGACGGCCCGCAGCTCA GATCAGTCATCATGTTGAGCATGGTGTGGTGGTG	5102
	CCAAGGTC**T**AGGAGCAG	5103
	CTGCTCCT**A**GACCTTGG	5104

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Zea mays* Arg4Term CGA-TGA	TCCTACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATGCACATC**T**GAGAAGAGGAGGCTACACCATCCACAGTAACAGGCATCATGTCGACCCTGACTTCGGCGG	5105
	CCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGTGTAGCCTCCTCTTCTC**A**GATGTGCATGCTCTTGTTCCTATCACACAGATTTTGAGGTCTGAAGGAGAAAAGGTAGGA	5106
	TGCACATC**T**GAGAAGAG	5107
	CTCTTCTC**A**GATGTGCA	5108
Male-sterile AG *Zea mays* Glu5Term GAA-TAA	TACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATGCACATCCGA**T**AAGAGGAGGCTACACCATCCACAGTAACAGGCATCATGTCGACCCTGACTTCGGCGGGGC	5109
	GCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGTGTAGCCTCCTCTT**A**TCGGATGTGCATGCTCTTGTTCCTATCACACAGATTTTGAGGTCTGAAGGAGAAAAGGTA	5110
	ACATCCGA**T**AAGAGGAG	5111
	CTCCTCTT**A**TCGGATGT	5112
Male-sterile AG *Zea mays* Glu6Term GAG-TAG	CTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATGCACATCCGAGAA**T**AGGAGGCTACACCATCCACAGTAACAGGCATCATGTCGACCCTGACTTCGGCGGGGCAGC	5113
	GCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGTGTAGCCTCCT**A**TTCTCGGATGTGCATGCTCTTGTTCCTATCACACAGATTTTGAGGTCTGAAGGAGAAAAG	5114
	TCCGAGAA**T**AGGAGGCT	5115
	AGCCTCCT**A**TTCTCGGA	5116
Male-sterile AG *Zea mays* Glu7Term GAG-TAG	TTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATGCACATCCGAGAAGAG**T**AGGCTACACCATCCACAGTAACAGGCATCATGTCGACCCTGACTTCGGCGGGGCAGCAGA	5117
	TCTGCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGTGTAGCCT**A**CTCTTCTCGGATGTGCATGCTCTTGTTCCTATCACACAGATTTTGAGGTCTGAAGGAGAA	5118
	GAGAAGAG**T**AGGCTACA	5119
	TGTAGCCT**A**CTCTTCTC	5120
Male-sterile AG *Oryza sativa* Lys5Term AAG-TAG	GCTGGGTCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGG**T**AGATCGAGATAAAGCGGATCGAGAACACGACGAACCGGCAGGTGACCTTCTGCAAGCGCC	5121
	GGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCTCGATCCGCTTTATCTCGATCT**A**CCCCCTCCCCATCTTCTCGCTGCTCCCCGCCGCCACCGCCGCCGACGATCCTGACCCAGC	5122
	GGAGGGGG**T**AGATCGAG	5123
	CTCGATCT**A**CCCCCTCC	5124

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Oryza sativa* Glu7Term GAG-TAG	TCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAGATC**T**AGATAAAGCGGATCGAGAACACGACGAACCGGCAGGTGACCTTCTGCAAGCGCCGCAATG	5125
	CATTGCGGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCTCGATCCGCTTTATCT**A**GATCTTCCCCCTCCCCATCTTCTCGCTGCTCCCCGCCGCCACCGCCGCCGACGATCCTGA	5126
	GGAAGATC**T**AGATAAAG	5127
	CTTTATCT**A**GATCTTCC	5128
Male-sterile AG *Oryza sativa* Lys9Term AAG-TAG	TCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAGATCGAGATA**T**AGCGGATCGAGAACACGACGAACCGGCAGGTGACCTTCTGCAAGCGCCGCAATGGCCTCC	5129
	GGAGGCCATTGCGGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCTCGATCCGCT**A**TATCTCGATCTTCCCCCTCCCCATCTTCTCGCTGCTCCCCGCCGCCACCGCCGCCGACGA	5130
	TCGAGATA**T**AGCGGATC	5131
	GATCCGCT**A**TATCTCGA	5132
Male-sterile AG *Oryza sativa* Glu12Term GAG-TAG	GCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAGATCGAGATAAAGCGGATC**T**AGAACACGACGAACCGGCAGGTGACCTTCTGCAAGCGCCGCAATGGCCTCCTGAAGAAGG	5133
	CCTTCTTCAGGAGGCCATTGCGGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCT**A**GATCCGCTTTATCTCGATCTTCCCCCTCCCCATCTTCTCGCTGCTCCCCGCCGCCACCGC	5134
	AGCGGATC**T**AGAACACG	5135
	CGTGTTCT**A**GATCCGCT	5136

Table 16
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Cucumis sativus* Tyr21Term TAT-TAG	GGGAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAGTTACATA**G**TCAAAGAGAAGAAATGGTATCATCAAAAAAGCCAAAGAAATTACTGTTCTTTGCGATGCT	5137
	AGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCATTTCTTCTCTTTGA**C**TATGTAACTTGTCTATTGCTTGAGTTCTCTATTCTTTTTATTTCTATTTTCCCTCTTCCC	5138

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTACATA**G**TCAAAGAG	5139
	CTCTTTGA**C**TATGTAAC	5140
Male-sterile PI *Cucumis sativus* Ser22Term TCA-TGA	GAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAGTTACATATT**G**AAAGAGAAGAAATGGTATCATCAAAAAAGCCAAAGAAATTACTGTTCTTTGCGATGCTCA	5141
	TGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCATTTCTTCTCTTT**C**AATATGTAACTTGTCTATTGCTTGAGTTCTCTATTCTTTTTATTTCTATTTTCCCTCTTC	5142
	TACATATT**G**AAAGAGAA	5143
	TTCTCTTT**C**AATATGTA	5144
Male-sterile PI *Cucumis sativus* Lys23Term AAG-TAG	AGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAGTTACATATTCA**T**AGAGAAGAAATGGTATCATCAAAAAAGCCAAAGAAATTACTGTTCTTTGCGATGCTCAAG	5145
	CTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCATTTCTTCTCT**A**TGAATATGTAACTTGTCTATTGCTTGAGTTCTCTATTCTTTTTATTTCTATTTTCCCTCT	5146
	CATATTCA**T**AGAGAAGA	5147
	TCTTCTCT**A**TGAATATG	5148
Male-sterile PI *Cucumis sativus* Arg24Term AGA-TGA	GGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAGTTACATATTCAAAG**T**GAAGAAATGGTATCATCAAAAAAGCCAAAGAAATTACTGTTCTTTGCGATGCTCAAGTTT	5149
	AAACTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCATTTCTTC**A**CTTTGAATATGTAACTTGTCTATTGCTTGAGTTCTCTATTCTTTTTATTTCTATTTTCCC	5150
	ATTCAAAG**T**GAAGAAAT	5151
	ATTTCTTC**A**CTTTGAAT	5152
Male-sterile PI *Malus domestica* Tyr21Term TAC-TAG	GGGACGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGGCAGGTGACCTA**G**TCCAAGAGGAGGAATGGGATTATCAAGAAGGCAAAGGAGATCACTGTTCTATGTGATGCT	5153
	AGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATCCCATTCCTCCTCTTGGA**C**TAGGTCACCTGCCTGTTACTTGAGTTCTCAATCCTCTTGATCTCAACCTTCCCACGTCCC	5154
	GTGACCTA**G**TCCAAGAG	5155
	CTCTTGGA**C**TAGGTCAC	5156

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Malus domestica* Lys23Term AAG-TAG	CGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGG CAGGTGACCTACTCC**T**AGAGGAGGAATGGGATTATCAAGAAGGCA AAGGAGATCACTGTTCTATGTGATGCTAAAG	5157
	CTTTAGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATC CCATTCCTCCTCT**A**GGAGTAGGTCACCTGCCTGTTACTTGAGTTCT CAATCCTCTTGATCTCAACCTTCCCACG	5158
	CCTACTCC**T**AGAGGAGG	5159
	CCTCCTCT**A**GGAGTAGG	5160
Male-sterile PI *Malus domestica* Lys30Term AAG-TAG	AGGATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGG AGGAATGGGATTATC**T**AGAAGGCAAAGGAGATCACTGTTCTATGTG ATGCTAAAGTATCTCTTATCATTTATTCTA	5161
	TAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGTGATC TCCTTTGCCTTCT**A**GATAATCCCATTCCTCCTCTTGGAGTAGGTCA CCTGCCTGTTACTTGAGTTCTCAATCCT	5162
	GGATTATC**T**AGAAGGCA	5163
	TGCCTTCT**A**GATAATCC	5164
Male-sterile PI *Malus domestica* Lys31Term AAG-TAG	ATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGGAGG AATGGGATTATCAAG**T**AGGCAAAGGAGATCACTGTTCTATGTGATG CTAAAGTATCTCTTATCATTTATTCTAGCT	5165
	AGCTAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGT GATCTCCTTTGCCT**A**CTTGATAATCCCATTCCTCCTCTTGGAGTAG GTCACCTGCCTGTTACTTGAGTTCTCAAT	5166
	TTATCAAG**T**AGGCAAAG	5167
	CTTTGCCT**A**CTTGATAA	5168
Male-sterile globosa *Antirrhinum majus* Gly2Term GGA-TGA	CATTTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAA AAACAAAAAAAATG**T**GAAGAGGAAAAATTGAGATCAAAAGAATTGAG AACTCAAGCAACAGGCAGGTTACTTACT	5169
	AGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATCTCA ATTTTTCCTCTTC**A**CATTTTTTTTGTTTTTGTTTTTCTCTCTTGTTTTTG TTTGCAGATAACTATTGTAAAAATG	5170
	AAAAAATG**T**GAAGAGGA	5171
	TCCTCTTC**A**CATTTTTT	5172
Male-sterile globosa *Antirrhinum majus* Arg3Term AGA-TGA	TTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAA CAAAAAAAATGGGA**T**GAGGAAAAATTGAGATCAAAAGAATTGAGAAC TCAAGCAACAGGCAGGTTACTTACTCAA	5173
	TTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATC TCAATTTTTCCTC**A**TCCCATTTTTTTTGTTTTTGTTTTTCTCTCTTGTT TTTGTTTGCAGATAACTATTGTAAAA	5174

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAATGGGATGAGGAAAA	5175
	TTTTCCTCATCCCATTT	5176
Male-sterile globosa *Antirrhinum majus* Gly4Term GGA-TGA	TACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAAAAATGGGAAGATGAAAAATTGAGATCAAAAGAATTGAGAACTCAAGCAACAGGCAGGTTACTTACTCAAAGA	5177
	TCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATCTCAATTTTTCATCTTCCCATTTTTTTGTTTTTGTTTTTCTCTCTTGTTTTTGTTTGCAGATAACTATTGTA	5178
	TGGGAAGATGAAAAATT	5179
	AATTTTTCATCTTCCCA	5180
Male-sterile globosa *Antirrhinum majus* Lys5Term AAA-TAA	AATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAAAAATGGGAAGAGGATAAATTGAGATCAAAAGAATTGAGAACTCAAGCAACAGGCAGGTTACTTACTCAAAGAGAA	5181
	TTCTCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATCTCAATTTATCCTCTTCCCATTTTTTTGTTTTTGTTTTTCTCTCTTGTTTTTGTTTGCAGATAACTATT	5182
	GAAGAGGATAAATTGAG	5183
	CTCAATTTATCCTCTTC	5184
Male-sterile PI *Zea mays* Lys5Term AAG-TAG	GCTGAGCTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCTAGATCAAGATCAAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCC	5185
	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTTGATCTTGATCTAGCCGCGCCCCATACTGCGTTCTCCACTCCCAAACAGATCCAAGGGCAGCAAGAGCTCAGC	5186
	GGCGCGGCTAGATCAAG	5187
	CTTGATCTAGCCGCGCC	5188
Male-sterile PI *Zea mays* Lys7Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5189
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTGCGTTCTCCACTCCCAAACAGATCCAAGGGCAGCAAGAG	5190
	GCAAGATCTAGATCAAG	5191
	CTTGATCTAGATCTTGC	5192

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Zea mays* Lys9Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5193
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTGCGTTCTCCACTCCCAAACAGATCCAAGGGCAGCAAGAG	5194
	GCAAGATCTAGATCAAG	5195
	CTTGATCTAGATCTTGC	5196
Male-sterile PI *Zea mays* Glu12Term GAG-TAG	GATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGATCAAGATCAAGAGGATCTAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	5197
	CCTTCTTGACCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTAGATCCTCTTGATCTTGATCTTGCCGCGCCCCATACTGCGTTCTCCACTCCCAAACAGATC	5198
	AGAGGATCTAGAACTCT	5199
	AGAGTTCTAGATCCTCT	5200
Male-sterile PI *Zea mays* Lys5Term AAG-TAG	GCTGAGCTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCTAGATCGAGATCAAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCC	5201
	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTTGATCTCGATCTAGCCGCGCCCCATACTCCGTTCTCCACTCCCTAACAGATTCAAGGGCAGCAAGAGCTCAGC	5202
	GGCGCGGCTAGATCGAG	5203
	CTCGATCTAGCCGCGCC	5204
Male-sterile PI *Zea mays* Glu7Term GAG-TAG	CTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5205
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTCCGTTCTCCACTCCCTAACAGATTCAAGGGCAGCAAGAG	5206
	GCAAGATCTAGATCAAG	5207
	CTTGATCTAGATCTTGC	5208
Male-sterile PI *Zea mays* Lys9Term AAG-TAG	CTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGATCGAGATCTAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCGGACTGG	5209
	CCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTAGATCTCGATCTTGCCGCGCCCCATACTCCGTTCTCCACTCCCTAACAGATTCAAGGGCAG	5210

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCGAGATC**T**AGAGGATC	5211
	GATCCTCT**A**GATCTCGA	5212
Male-sterile PI *Zea mays* Glu12Term GAG-TAG	AATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGATCGAGATCAAGAGGATC**T**AGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	5213
	CCTTCTTGACCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCT**A**GATCCTCTTGATCTCGATCTTGCCGCGCCCCATACTCCGTTCTCCACTCCCTAACAGATT	5214
	AGAGGATC**T**AGAACTCT	5215
	AGAGTTCT**A**GATCCTCT	5216
Male-sterile PI *Oryza sativa* Lys5Term AAG-TAG	TTGCTGCTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGG**T**AGATCGAGATCAAGAGGATCGAGAACTCCACCAACCGCCAGGTGACCTTCTCCAAGCGCA	5217
	TGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCCTCTTGATCTCGATCT**A**CCCGCGCCCCATCCCGCCTCCTCCTCCTCCTCCTTCCTCCAGCTAGCTTAGCAGCAA	5218
	GGCGCGGG**T**AGATCGAG	5219
	CTCGATCT**A**CCCGCGCC	5220
Male-sterile PI *Oryza sativa* Glu7Term GAG-TAG	CTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAGATC**T**AGATCAAGAGGATCGAGAACTCCACCAACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCG	5221
	CGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCCTCTTGATCT**A**GATCTTCCCGCGCCCCATCCCGCCTCCTCCTCCTCCTCCTTCCTCCAGCTAGCTTAG	5222
	GGAAGATC**T**AGATCAAG	5223
	CTTGATCT**A**GATCTTCC	5224
Male-sterile PI *Oryza sativa* Lys9Term AAG-TAG	TAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAGATCGAGATC**T**AGAGGATCGAGAACTCCACCAACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCGGGATCC	5225
	GGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCCTCT**A**GATCTCGATCTTCCCGCGCCCCATCCCGCCTCCTCCTCCTCCTCCTCCTTCCTCCAGCTA	5226
	TCGAGATC**T**AGAGGATC	5227
	GATCCTCT**A**GATCTCGA	5228

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Oryza sativa* Glu12Term GAG-TAG	GAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAGATCGAGATCAAGAGGATC**T**AGAACTCCACCAACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCGGGATCCTCAAGAAGG	5229
	CCTTCTTGAGGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCT**A**GATCCTCTTGATCTCGATCTTCCCGCGCCCCATCCCGCCTCCTCCTCCTCCTCCTCCTTC	5230
	AGAGGATC**T**AGAACTCC	5231
	GGAGTTCT**A**GATCCTCT	5232

Example 7

Engineering plants for abiotic stress tolerance

Environmental stresses, such as drought, increased soil salinity, soil contamination with heavy metals, and extreme temperature, are major factors limiting plant growth and productivity. The worldwide loss in yield of three major cereal crops, rice, maize, and wheat due to water stress (drought) has been estimated to be over ten billion dollars annually and many currently marginal soils could be brought into cultivation if suitable plant varieties were available.

Physiological and biochemical responses to high levels of ionic or nonionic solutes and decreased water potential have been studied in a variety of plants. It is known, for example, that increasing levels of alcohol dehydrogenase can confer enhances flooding resistance in plants. There are also several possible mechanisms to enhance plant salt tolerance. For example, one mechanism underlying the adaptation or tolerance of plants to osmotic stresses is the accumulation of compatible, low molecular weight osmolytes such as sugar alcohols, special amino acids, and glycinebetaine. Such accumulation can be engineered, for example, by removing feedback inhibition on 1-pyrroline-t-carboxylate synthetase, which results in accumulation of proline. Additionally, recent experiments suggest that altering the expression or activity of specific sodium or potassium transporters can confer enhanced salt tolerance.

Plant tolerance of contamination by heavy metals such as lead and aluminum in soils has also been investigated and one mechanism underlying tolerance is the production of dicarboxylic acids such as oxalate and citrate. In addition, individual genes involved in heavy metal sensitivity have been identified.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer stress tolerance in plants.

Table 17
Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance P5CS *Arabidopsis thaliana* Phe128Ala TTT-GCT	CGTCTTTTTGTGTGGTAGTTGGATGTGACGGTTGCTCAAATGCTT GTGACCGATAGCAGT**GC**TAGAGATAAGGATTTCAGGAAGCAACTT AGTGAAACTGTCAAAGCGATGCTGAGGATGA	5233
	TCATCCTCAGCATCGCTTTGACAGTTTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTA**GC**ACTGCTATCGGTCACAAGCATTTGAGCAACC GTCACATCCAACTACCACACAAAAAGACG	5234
	ATAGCAGT**GC**TAGAGAT	5235
	ATCTCTA**GC**ACTGCTAT	5236
Salt Tolerance P5CS 1 *Brassica napus* Phe128Ala TTC-GCC	GAGACTATGTTTGACCAGCTGGATGTGACGGCTGCTCAGCTGCTG GTGAATGACAGTAGT**GC**CAGAGACAAGGAGTTCAGGAAGCAACTT AATGAGACAGTGAAGTCCATGCTTGATTTGA	5237
	TCAAATCAAGCATGGACTTCACTGTCTCATTAAGTTGCTTCCTGAA CTCCTTGTCTCTG**GC**ACTACTGTCATTCACCAGCAGCTGAGCAGC CGTCACATCCAGCTGGTCAAACATAGTCTC	5238
	ACAGTAGT**GC**CAGAGAC	5239
	GTCTCTG**GC**ACTACTGT	5240
Salt Tolerance P5CS 2 *Brassica napus* Phe129Ala TTC-GCC	GAGACTATGTTTGACCAGATGGATGTGACGGTGGCTCAAATGCTG GTGACTGATAGCAGT**G**TCAGAGATAAGGATTTCAGGAAGCAACTT AGTGAGACAGTCAAAGCTATGCTGAAAATGA	5241
	TCATTTTCAGCATAGCTTTGACTGTCTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTGA**C**ACTGCTATCAGTCACCAGCATTTGAGCCACC GTCACATCCATCTGGTCAAACATAGTCTC	5242
	ATAGCAGT**G**TCAGAGAT	5243
	ATCTCTGA**C**ACTGCTAT	5244
Salt Tolerance P5CS *Oryza sativa* Phe128Ala TTT-GCT	GATATGTTGTTTAACCAACTGGATGTCTCGTCATCTCAACTTCTTG TCACCGACAGTGAT**GC**TGAGAACCCAAAGTTCCGGGAGCAACTCA CTGAAACTGTTGAGTCATTATTAGATCTTA	5245
	TAAGATCTAATAATGACTCAACAGTTTCAGTGAGTTGCTCCCGGAA CTTTGGGTTCTCA**GC**ATCACTGTCGGTGACAAGAAGTTGAGATGA CGAGACATCCAGTTGGTTAAACAACATATC	5246
	ACAGTGAT**GC**TGAGAAC	5247
	GTTCTCA**GC**ATCACTGT	5248

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance P5CS *Medicago sativa* Phe128Ala TTT-GCT	GATATTTTGTTTAGTCAGCTGGATGTGACATCTGCTCAGCTTCTTGTTACTGACAATGAT**GC**TAGAGACCAAGATTTTAGAAAGCAACTTTCTGAAACTGTGAGATCACTTCTAGCACTAA	5249
	TTAGTGCTAGAAGTGATCTCACAGTTTCAGAAAGTTGCTTTCTAAAATCTTGGTCTCTA**GC**ATCATTGTCAGTAACAAGAAGCTGAGCAGATGTCACATCCAGCTGACTAAACAAAATATC	5250
	ACAATGAT**GC**TAGAGAC	5251
	GTCTCTA**GC**ATCATTGT	5252
Salt Tolerance P5CS *Actinidia deliciosa* Phe128Ala TTT-GCT	GATACATTGTTTAGTCAGCTGGATGTGACATCAGCTCAGCTACTCGTTACTGATAATGAT**GC**TAGGGATCCAGAATTCAGGAAGCAACTTACTGAAACTGTAGAATCACTATTGAATTTGA	5253
	TCAAATTCAATAGTGATTCTACAGTTTCAGTAAGTTGCTTCCTGAATTCTGGATCCCTA**GC**ATCATTATCAGTAACGAGTAGCTGAGCTGATGTCACATCCAGCTGACTAAACAATGTATC	5254
	ATAATGAT**GC**TAGGGAT	5255
	ATCCCTA**GC**ATCATTAT	5256
Salt Tolerance P5CS *Cichorium intybus* Phe122Ala TTC-GCC	GACACACTCTTCAGTCAACTGGATGTGACATCAGCACAGCTTCTTGTAACAGATAATGAC**GC**CAGAAGTCCAGAATTTAGAAAACAACTTACTGAAACAGTCGATTCTTTATTATCTTATA	5257
	TATAAGATAATAAAGAATCGACTGTTTCAGTAAGTTGTTTTCTAAATTCTGGACTTCTG**GC**GTCATTATCTGTTACAAGAAGCTGTGCTGATGTCACATCCAGTTGACTGAAGAGTGTGTC	5258
	ATAATGAC**GC**CAGAAGT	5259
	ACTTCTG**GC**GTCATTAT	5260
Salt Tolerance P5CS *Lycopersicon esculentum* Phe128Ala TTT-GCT	GATTCTTTGTTCAGTCAGTTGGATGTGACATCAGCTCAGCTTCTGGTGACTGATAATGAC**GC**TAGAGATCCAGATTTTAGGAGACAACTCAATGACACAGTAAATTCGTTGCTTTCTCTAA	5261
	TTAGAGAAAGCAACGAATTTACTGTGTCATTGAGTTGTCTCCTAAAATCTGGATCTCTA**GC**GTCATTATCAGTCACCAGAAGCTGAGCTGATGTCACATCCAACTGACTGAACAAAGAATC	5262
	ATAATGAC**GC**TAGAGAT	5263
	ATCTCTA**GC**GTCATTAT	5264
Salt Tolerance P5CS *Vigna unguiculata* Phe162Ala TTT-GCT	GATACCATGTTCAGCCAGCTTGATGTGACTTCTTCCCAACTTCTTGTGAATGATGGATTT**GC**TAGGGATGCTGGCTTCAGAAAACAACTTTCGGACACAGTGAACGCGTTATTAGATTTAA	5265
	TTAAATCTAATAACGCGTTCACTGTGTCCGAAAGTTGTTTTCTGAAGCCAGCATCCCTA**GC**AAATCCATCATTCACAAGAAGTTGGGAAGAAGTCACATCAAGCTGGCTGAACATGGTATC	5266
	ATGGATTT**GC**TAGGGAT	5267

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATCCCTA**GC**AAATCCAT	5268
Salt Tolerance P5CS *Mesembryanthemum crystallinum* Phe125Ala TTT-GCT	GACACCTTGTTTAGTCAGTTGGATCTGACTGCTGCTCAGCTGCTT GTGACGGACAACGAC**GC**TAGAGATCCAAGTTTTAGAACACAACTA ACTGAAACAGTGTATCAGTTGTTGGATCTAA	5269
	TTAGATCCAACAACTGATACACTGTTTCAGTTAGTTGTGTTCTAAAA CTTGGATCTCTA**GC**GTCGTTGTCCGTCACAAGCAGCTGAGCAGCA GTCAGATCCAACTGACTAAACAAGGTGTC	5270
	ACAACGAC**GC**TAGAGAT	5271
	ATCTCTA**GC**GTCGTTGT	5272
Salt Tolerance P5CS *Vitis vinifera* Phe130Ala TTT-GCT	GACACATTATTTAGCCAGCTGGATGTGACATCAGCTCAGCTTCTT GTGACTGATAATGAT**GC**TAGGGATGAAGCTTTCCGAAATCAACTTA CTCAAACAGTGGATTCATTGTTAGCTTTGA	5273
	TCAAAGCTAACAATGAATCCACTGTTTGAGTAAGTTGATTTCGGAA AGCTTCATCCCTA**GC**ATCATTATCAGTCACAAGAAGCTGAGCTGAT GTCACATCCAGCTGGCTAAATAATGTGTC	5274
	ATAATGAT**GC**TAGGGAT	5275
	ATCCCTA**GC**ATCATTAT	5276
Salt Tolerance P5CS *Vigna aconitifolia* Phe129Ala TTT-GCT	GATACGCTGTTCACTCAGCTCGATGTGACATCGGCTCAGCTTCTT GTGACGGATAACGAT**GC**TCGAGATAAGGATTTCAGGAAGCAGCTT ACTGAGACTGTGAAGTCGCTGTTGGCGCTGA	5277
	TCAGCGCCAACAGCGACTTCACAGTCTCAGTAAGCTGCTTCCTGA AATCCTTATCTCGA**GC**ATCGTTATCCGTCACAAGAAGCTGAGCCG ATGTCACATCGAGCTGAGTGAACAGCGTATC	5278
	ATAACGAT**GC**TCGAGAT	5279
	ATCTCGA**GC**ATCGTTAT	5280
Salt Tolerance HKT1 *Arabidopsis thaliana* Ser207Val TCC-GTC	AGAGATGTTCTTAGTTCCAAAGAAATCTCACCTCTCACTTTCTCCG TCTTCACAACAGTT**GT**CACGTTTGCAAACTGCGGATTTGTCCCCAC GAATGAGAACATGATCATCTTTCGCAAAA	5281
	TTTTGCGAAAGATGATCATGTTCTCATTCGTGGGGACAAATCCGCA GTTTGCAAACGTG**AC**AACTGTTGTGAAGACGGAGAAAGTGAGAGG TGAGATTTCTTTGGAACTAAGAACATCTCT	5282
	CAACAGTT**GT**CACGTTT	5283
	AAACGTG**AC**AACTGTTG	5284
Salt Tolerance HKT1 *Arabidopsis thaliana* Gln237Leu CAA-CTA	CGAATGAGAACATGATCATCTTTCGCAAAAACTCTGGTCTCATCTG GCTCCTAATCCCTC**T**AGTACTGATGGGAAACACTTTGTTCCCTTGC TTCTTGGTTTTGCTCATATGGGGACTTTA	5285
	TAAAGTCCCCATATGAGCAAAACCAAGAAGCAAGGGAACAAAGTG TTTCCCATCAGTACT**A**GAGGGATTAGGAGCCAGATGAGACCAGAG TTTTTGCGAAAGATGATCATGTTCTCATTCG	5286

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCCCTC**T**AGTACTGA	5287
	TCAGTACT**A**GAGGGATT	5288
Salt Tolerance HKT1 *Arabidopsis thaliana* Asn332Ser AAT-AGT	AGTCTCTAGAAGGAATGAGTTCGTACGAGAAGTTGGTTGGATCGT TGTTTCAAGTGGTGA**G**TTCGCGACACACCGGAGAAACTATAGTAG ACCTCTCTACACTTTCCCCAGCTATCTTGGT	5289
	ACCAAGATAGCTGGGGAAAGTGTAGAGAGGTCTACTATAGTTTCT CCGGTGTGTCGCGAA**C**TCACCACTTGAAACAACGATCCAACCAAC TTCTCGTACGAACTCATTCCTTCTAGAGACT	5290
	AGTGGTGA**G**TTCGCGAC	5291
	GTCGCGAA**C**TCACCACT	5292
Salt Tolerance HKT1 *Eucalyptus camaldulensis* Ser256Val TCG-GTG	AGAGATGTGCTAAAGAAGAAAGGTCTCAAAATGGTGACCTTTTCC GTCTTCACCACCGTG**GT**GACCTTTGCCAGTTGTGGGTTTGTCCCG ACCAATGAAAACATGATTATCTTCAGCAAAA	5293
	TTTTGCTGAAGATAATCATGTTTTCATTGGTCGGGACAAACCCACA ACTGGCAAAGGTC**AC**CACGGTGGTGAAGACGGAAAAGGTCACCA TTTTGAGACCTTTCTTCTTTAGCACATCTCT	5294
	CCACCGTG**GT**GACCTTT	5295
	AAAGGTC**AC**CACGGTGG	5296
Salt Tolerance HKT1 *Eucalyptus camaldulensis* Gln286Leu CAG-CTG	CCAATGAAAACATGATTATCTTCAGCAAAAACTCTGGCCTCCTCCT GATTCTCATCCCTC**T**GGCCCTTCTTGGGAACATGCTGTTCCCATC GAGCCTACGTTTGACGCTTTGGCTCATCGG	5297
	CCGATGAGCCAAAGCGTCAAACGTAGGCTCGATGGGAACAGCAT GTTCCCAAGAAGGGCC**A**GAGGGATGAGAATCAGGAGGAGGCCA GAGTTTTTGCTGAAGATAATCATGTTTTCATTGG	5298
	CATCCCTC**T**GGCCCTTC	5299
	GAAGGGCC**A**GAGGGATG	5300
Salt Tolerance HKT1 *Eucalyptus camaldulensis* Asn381Ser AAC-AGC	AATCGTTGAATGGACTAAGCTCCTGTGAGAAAATCGTGGGCGCGC TGTTTCAGTGCGTGA**G**CAGCAGACATACCGGCGAGACGGTCGTC GATCTGTCCACAGTTGCTCCCGCCATCTTGGT	5301
	ACCAAGATGGCGGGAGCAACTGTGGACAGATCGACGACCGTCTC GCCGGTATGTCTGCTG**C**TCACGCACTGAAACAGCGCGCCCACGA TTTTCTCACAGGAGCTTAGTCCATTCAACGATT	5302
	GTGCGTGA**G**CAGCAGAC	5303
	GTCTGCTG**C**TCACGCAC	5304

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance HKT1 *Oryza sativa* Ser238Val TCC-GTC	AAAGCTCCACTGAAGAAGAAAGGGATCAACATTGCACTCTTCTCATTCTCGGTCACGGTCGTCTCGTTTGCGAATGTGGGGCTCGTGCCGACAAATGAGAACATGGCAATCTTCTCCAAGA	5305
	TCTTGGAGAAGATTGCCATGTTCTCATTTGTCGGCACGAGCCCCACATTCGCAAACGAGACGACCGTGACCGAGAATGAGAAGAGTGCAATGTTGATCCCTTTCTTCTTCAGTGGAGCTTT	5306
	TCACGGTCGTCTCGTTT	5307
	AAACGAGACGACCGTGA	5308
Salt Tolerance HKT1 *Oryza sativa* Gln268Leu CAG-CTG	CAAATGAGAACATGGCAATCTTCTCCAAGAACCCGGGCCTCCTCCTCCTGTTCATCGGCCTGATTCTTGCAGGCAATACACTTTACCCTCTCTTCCTAAGGCTATTGATATGGTTCCTGGG	5309
	CCCAGGAACCATATCAATAGCCTTAGGAAGAGAGGGTAAAGTGTATTGCCTGCAAGAATCAGGCCGATGAACAGGAGGAGGAGGCCCGGGTTCTTGGAGAAGATTGCCATGTTCTCATTTG	5310
	CATCGGCCTGATTCTTG	5311
	CAAGAATCAGGCCGATG	5312
Salt Tolerance HKT1 *Oryza sativa* Asn363Ser AAC-AGC	CAGTCTTTGATGGACTCAGCTCTTACCAGAAGATTATCAATGCATTGTTCATGGCAGTGAGCGCAAGGCACTCGGGGGAGAACTCCATCGACTGCTCACTCATCGCCCCTGCTGTTCTAGT	5313
	ACTAGAACAGCAGGGGCGATGAGTGAGCAGTCGATGGAGTTCTCCCCCGAGTGCCTTGCGCTCACTGCCATGAACAATGCATTGATAATCTTCTGGTAAGAGCTGAGTCCATCAAAGACTG	5314
	GGCAGTGAGCGCAAGGC	5315
	GCCTTGCGCTCACTGCC	5316
Salt Tolerance HKT1 *Triticum aestivum* Ala240Val GCC-GTC	GTGCCCCACTGAACAAGAAAGGGATCAACATCGTGCTCTTCTCACTATCAGTCACCGTTGTCTCCTGTGCGAATGCAGGACTCGTGCCCACAAATGAGAACATGGTCATCTTCTCAAAGAA	5317
	TTCTTTGAGAAGATGACCATGTTCTCATTTGTGGGCACGAGTCCTGCATTCGCACAGGAGACAACGGTGACTGATAGTGAGAAGAGCACGATGTTGATCCCTTTCTTGTTCAGTGGGGCAC	5318
	CACCGTTGTCTCCTGTG	5319
	CACAGGAGACAACGGTG	5320
Salt Tolerance HKT1 *Triticum aestivum* Gln270Leu CAG-CTG	CAAATGAGAACATGGTCATCTTCTCAAAGAATTCAGGCCTCTTGTTGCTGCTGAGTGGCCTGATGCTCGCAGGCAATACATTGTTCCCTCTCTTCCTGAGGCTACTGGTGTGGTTCCTGGG	5321
	CCCAGGAACCACACCAGTAGCCTCAGGAAGAGAGGGAACAATGTATTGCCTGCGAGCATCAGGCCACTCAGCAGCAACAAGAGGCCTGAATTCTTTGAGAAGATGACCATGTTCTCATTTG	5322
	GAGTGGCCTGATGCTCG	5323

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGAGCATC**A**GGCCACTC	5324
Salt Tolerance HKT1 *Triticum aestivum* Asn365Ser AAT-AGT	CAGTCTTTGATGGGCTCAGCTCTTATCAGAAGACTGTCAATGCATT CTTCATGGTGGTGA**G**TGCGAGGCACTCAGGGGAGAATTCCATCG ACTGCTCGCTCATGTCCCCTGCCATTATAGT	5325
	ACTATAATGGCAGGGGACATGAGCGAGCAGTCGATGGAATTCTCC CCTGAGTGCCTCGCA**C**TCACCACCATGAAGAATGCATTGACAGTC TTCTGATAAGAGCTGAGCCCATCAAAGACTG	5326
	GGTGGTGA**G**TGCGAGGC	5327
	GCCTCGCA**C**TCACCACC	5328
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Arg7Term CGA-TGA	TTTTTTTTGTTTTCGTTTTCAAAAACAAAATCTTTGAATTTTATGGCA ACCCGTCTTCTC**T**GAACAAACTTTATCCGGCGATCTTACCGTTTAC CCGCTTTTAGCCCGGTGGGTCCTCCCA	5329
	TGGGAGGACCCACCGGGCTAAAAGCGGGTAAACGGTAAGATCGC CGGATAAAGTTTGTTC**A**GAGAAGACGGGTTGCCATAAAATTCAAA GATTTTGTTTTTGAAAACGAAAACAAAAAAAA	5330
	GTCTTCTC**T**GAACAAAC	5331
	GTTTGTTC**A**GAGAAGAC	5332
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Arg13Term CGA-TGA	TCAAAAACAAAATCTTTGAATTTTATGGCAACCCGTCTTCTCAGAA CAAACTTTATCCGG**T**GATCTTACCGTTTACCCGCTTTTAGCCCGGT GGGTCCTCCCACCGTGACTGCTTCCACCG	5333
	CGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAAGC GGGTAAACGGTAAGATC**A**CCGGATAAAGTTTGTTCTGAGAAGACG GGTTGCCATAAAATTCAAAGATTTTGTTTTTGA	5334
	TTATCCGG**T**GATCTTAC	5335
	GTAAGATC**A**CCGGATAA	5336
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Tyr15Term TAC-TAG	AAAATCTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAAACTTTA TCCGGCGATCTTA**G**CGTTTACCCGCTTTTAGCCCGGTGGGTCCTC CCACCGTGACTGCTTCCACCGCCGTCGTC	5337
	GACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGG CTAAAAGCGGGTAAACG**C**TAAGATCGCCGGATAAAGTTTGTTCGG AGAAGACGGGTTGCCATAAAATTCAAAGATTTT	5338
	CGATCTTA**G**CGTTTACC	5339
	GGTAAACG**C**TAAGATCG	5340

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Leu17Term TTA-TAA	CTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAAACTTTATCCG GCGATCTTACCGTT**A**ACCCGCTTTTAGCCCGGTGGGTCCTCCCAC CGTGACTGCTTCCACCGCCGTCGTCCCGGA	5341
	TCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCA CCGGGCTAAAAGCGGGT**T**AACGGTAAGATCGCCGGATAAAGTTTG TTCGGAGAAGACGGGTTGCCATAAAATTCAAAG	5342
	TTACCGTT**A**ACCCGCTT	5343
	AAGCGGGT**T**AACGGTAA	5344
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Gly42Term GGA-TGA	CCGGTGGGTCCTCCCACCGTGACTGCTTCCACCGCCGTCGTCCC GGAGATTCTCTCCTTT**T**GACAACAAGCACCGGAACCACCTCTTCA CCACCCAAAACCCACCGAGCAATCTCACGATG	5345
	CATCGTGAGATTGCTCGGTGGGTTTTGGGTGGTGAAGAGGTGGT TCCGGTGCTTGTTGTC**A**AAAGGAGAGAATCTCCGGGACGACGGC GGTGGAAGCAGTCACGGTGGGAGGACCCACCGG	5346
	TCTCCTTT**T**GACAACAA	5347
	TTGTTGTC**A**AAAGGAGA	5348
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Arg4Term CGA-TGA	ACATGAAGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCA AACTATGAATTTC**T**GACAAGAGAAGTTTGTAAGGTCAGTGTTCCAG ATTTGTCTCATTGAATTCTAAGTCGTGA	5349
	TCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTAC AAACTTCTCTTGTC**A**GAAATTCATAGTTTGAGACTAATAAGATTCAA TACAAACAGAGATTTCACTGCTTCATGT	5350
	TGAATTTC**T**GACAAGAG	5351
	CTCTTGTC**A**GAAATTCA	5352
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Gln5Term CAA-TAA	TGAAGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAAC TATGAATTTCCGA**T**AAGAGAAGTTTGTAAGGTCAGTGTTCCAGATT TGTCTCATTGAATTCTAAGTCGTGAAGC	5353
	GCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCT TACAAACTTCTCTT**A**TCGGAAATTCATAGTTTGAGACTAATAAGATT CAATACAAACAGAGATTTCACTGCTTCA	5354
	ATTTCCGA**T**AAGAGAAG	5355
	CTTCTCTT**A**TCGGAAAT	5356
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Glu6Term GAG-TAG	AGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACTAT GAATTTCCGACAA**T**AGAAGTTTGTAAGGTCAGTGTTCCAGATTTGT CTCATTGAATTCTAAGTCGTGAAGCTTA	5357
	TAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGA CCTTACAAACTTCT**A**TTGTCGGAAATTCATAGTTTGAGACTAATAA GATTCAATACAAACAGAGATTTCACTGCT	5358

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACAA**T**AGAAGTTT	5359
	AAACTTCT**A**TTGTCGGA	5360
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Lys7Term AAG-TAG	AGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACTATGAATTTCCGACAAGAG**T**AGTTTGTAAGGTCAGTGTTCCAGATTTGTCTCATTGAATTCTAAGTCGTGAAGCTTAATT	5361
	AATTAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTACAAACT**A**CTCTTGTCGGAAATTCATAGTTTGAGACTAATAAGATTCAATACAAACAGAGATTTCACT	5362
	GACAAGAG**T**AGTTTGTA	5363
	TACAAACT**A**CTCTTGTC	5364
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Gln12Term CAA-TAA	CATTGAATTCTAAGTCGTGAAGCTTAATTCGATTCTTCTTCACTTTCTCGGATCAGGTTT**T**AAGATTGGAAGTCGGATAAGACTTCCTCCGACGTGGAATATTCCGGTAAAAACGAGATTC	5365
	GAATCTCGTTTTTACCGGAATATTCCACGTCGGAGGAAGTCTTATCCGACTTCCAATCTT**A**AAACCTGATCCGAGAAAGTGAAGAAGAATCGAATTAAGCTTCACGACTTAGAATTCAATG	5366
	TCAGGTTT**T**AAGATTGG	5367
	CCAATCTT**A**AAACCTGA	5368
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gln5Term CAA-TAA	TGGAAGTCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGC**T**AAGACGAGTTTGTGAGGTTTCAGGATTGGAAATCAGAGAGAAGCTCTGAGGGAAATTTTC	5369
	GAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCTGAAACCTCACAAACTCGTCTT**A**GCGGTGATTCATAACTTTAGCCAATGCATCAACCTGCTCAACGTGGGGGATTGACTTCCA	5370
	ATCACCGC**T**AAGACGAG	5371
	CTCGTCTT**A**GCGGTGAT	5372
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gly7Term GAG-TAG	TCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGAC**T**AGTTTGTGAGGTTTCAGGATTGGAAATCAGAGAGAAGCTCTGAGGGAAATTTTCATGCTA	5373
	TAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCTGAAACCTCACAAACT**A**GTCTTGGCGGTGATTCATAACTTTAGCCAATGCATCAACCTGCTCAACGTGGGGGATTGA	5374
	GCCAAGAC**T**AGTTTGTG	5375
	CACAAACT**A**GTCTTGGC	5376

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gln12Term CAG-TAG	GAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTGAGGTTT**T**AGGATTGGAAATCAGAGAGAAGCTCTGAGGGAAATTTTCATGCTAAAGGTGGAGTCCACC	5377
	GGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCT**A**AAACCTCACAAACTCGTCTTGGCGGTGATTCATAACTTTAGCCAATGCATCAACCTGCTC	5378
	TGAGGTTT**T**AGGATTGG	5379
	CCAATCCT**A**AAACCTCA	5380
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Trp14Term TGG-TGA	TGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTGAGGTTTCAGGATTG**T**AAATCAGAGAGAAGCTCTGAGGGAAATTTTCATGCTAAAGGTGGAGTCCACCGAAGTAAA	5381
	TTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTT**A**CAATCCTGAAACCTCACAAACTCGTCTTGGCGGTGATTCATAACTTTAGCCAATGCATCA	5382
	CAGGATTG**T**AAATCAGA	5383
	TCTGATTT**A**CAATCCTG	5384
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Lys15Term AAA-TAA	GATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTGAGGTTTCAGGATTGG**T**AATCAGAGAGAAGCTCTGAGGGAAATTTTCATGCTAAAGGTGGAGTCCACCGAAGTAAAG	5385
	CTTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATT**A**CCAATCCTGAAACCTCACAAACTCGTCTTGGCGGTGATTCATAACTTTAGCCAATGCATC	5386
	AGGATTGG**T**AATCAGAG	5387
	CTCTGATT**A**CCAATCCT	5388
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Glu2Term GAA-TAA	CTTGAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAGATAATGATG**T**AAAGAGAGGACAGATATGTTAGATTTCAGGACTGCAAATCAGAGCAATCTGTTATCTCAG	5389
	CTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAACATATCTGTCCTCTCTTT**A**CATCATTATCTCCACCAGGCGAACAGTTAGCAGCTAAGAGTGGTAGATCAATTCTTCAAG	5390
	TAATGATG**T**AAAGAGAG	5391
	CTCTCTTT**A**CATCATTA	5392

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Arg3Term AGA-TGA	GAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTG GAGATAATGATGGAA**T**GAGAGGACAGATATGTTAGATTTCAGGAC TGCAAATCAGAGCAATCTGTTATCTCAGAGA	5393
	TCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAAC ATATCTGTCCTCTC**A**TTCCATCATTATCTCCACCAGGCGAACAGTT AGCAGCTAAGAGTGGTAGATCAATTCTTC	5394
	TGATGGAA**T**GAGAGGAC	5395
	GTCCTCTC**A**TTCCATCA	5396
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Glu4Term GAG-TAG	GAATTGATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAG ATAATGATGGAAAGA**T**AGGACAGATATGTTAGATTTCAGGACTGCA AATCAGAGCAATCTGTTATCTCAGAGAACG	5397
	CGTTCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCT AACATATCTGTCCT**A**TCTTTCCATCATTATCTCCACCAGGCGAACA GTTAGCAGCTAAGAGTGGTAGATCAATTC	5398
	TGGAAAGA**T**AGGACAGA	5399
	TCTGTCCT**A**TCTTTCCA	5400
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Arg6Term AGA-TGA	ATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAGATAATG ATGGAAAGAGAGGAC**T**GATATGTTAGATTTCAGGACTGCAAATCA GAGCAATCTGTTATCTCAGAGAACGCAGTTT	5401
	AAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTG AAATCTAACATATC**A**GTCCTCTCTTTCCATCATTATCTCCACCAGG CGAACAGTTAGCAGCTAAGAGTGGTAGAT	5402
	GAGAGGAC**T**GATATGTT	5403
	AACATATC**A**GTCCTCTC	5404
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Tyr7Term TAT-TAG	CCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAGATAATGATGGA AAGAGAGGACAGATA**G**GTTAGATTTCAGGACTGCAAATCAGAGCA ATCTGTTATCTCAGAGAACGCAGTTTCACCA	5405
	TGGTGAAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTTGCAG TCCTGAAATCTAAC**C**TATCTGTCCTCTCTTTCCATCATTATCTCCAC CAGGCGAACAGTTAGCAGCTAAGAGTGG	5406
	GACAGATA**G**GTTAGATT	5407
	AATCTAAC**C**TATCTGTC	5408
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Glu2Term GAG-TAG	ATCCTTCTCTGAGAAAAAACAACAGATCCGAATTTTATCTTTAATCA GCCGGAAAAAATG**T**AGAAAGCGATCGAGAGACAACGCGTTCTTCT TGAGCATCTCCGACCTTCTTCTTCTTCTT	5409
	AAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTTGTC TCTCGATCGCTTTCT**A**CATTTTTTCCGGCTGATTAAAGATAAAATTC GGATCTGTTGTTTTTTCTCAGAGAAGGAT	5410

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAAATG**T**AGAAAGCG	5411
	CGCTTTCT**A**CATTTTTT	5412
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Lys3Term AAA-TAA	CTTCTCTGAGAAAAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAG**T**AAGCGATCGAGAGACAACGCGTTCTTCTTGAGCATCTCCGACCTTCTTCTTCTTCTTCGC	5413
	GCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTTGTCTCTCGATCGCTT**A**CTCCATTTTTTCCGGCTGATTAAAGATAAAATTCGGATCTGTTGTTTTTTCTCAGAGAAG	5414
	AAATGGAG**T**AAGCGATC	5415
	GATCGCTT**A**CTCCATTT	5416
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Glu6Term GAG-TAG	GAAAAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGAAAGCGATC**T**AGAGACAACGCGTTCTTCTTGAGCATCTCCGACCTTCTTCTTCTTCTTCGCACAATTACG	5417
	CGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTTGTCTCT**A**GATCGCTTTCTCCATTTTTTCCGGCTGATTAAAGATAAAATTCGGATCTGTTGTTTTTTC	5418
	AAGCGATC**T**AGAGACAA	5419
	TTGTCTCT**A**GATCGCTT	5420
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Arg7Term AGA-TGA	AAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGAAAGCGATCGAG**T**GACAACGCGTTCTTCTTGAGCATCTCCGACCTTCTTCTTCTTCTTCGCACAATTACGAGG	5421
	CCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTTGTC**A**CTCGATCGCTTTCTCCATTTTTTCCGGCTGATTAAAGATAAAATTCGGATCTGTTGTTTT	5422
	CGATCGAG**T**GACAACGC	5423
	GCGTTGTC**A**CTCGATCG	5424
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Gln8Term CAA-TAA	ACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGAAAGCGATCGAGAGA**T**AACGCGTTCTTCTTGAGCATCTCCGACCTTCTTCTTCTTCTTCGCACAATTACGAGGCTT	5425
	AAGCCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTT**A**TCTCTCGATCGCTTTCTCCATTTTTTCCGGCTGATTAAAGATAAAATTCGGATCTGTTGT	5426
	TCGAGAGA**T**AACGCGTT	5427
	AACGCGTT**A**TCTCTCGA	5428

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Glu26Term GAA-TAA	GAGAGACAAAGAGTTCTTCTTGAACATCTCCGTCCTTCTTCTTCTTCCTCTCACAGCTTT**T**AAGGCTCTCTCTCTGCTTCAGCTTGCTTGGCTGGGGACAGTGCTGCGTATCAGAGGACCT	5429
	AGGTCCTCTGATACGCAGCACTGTCCCCAGCCAAGCAAGCTGAAGCAGAGAGAGAGCCTT**A**AAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGATGTTCAAGAAGAACTCTTTGTCTCTC	5430
	ACAGCTTT**T**AAGGCTCT	5431
	AGAGCCTT**A**AAAGCTGT	5432
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Ser32Term TCA-TGA	TTGAACATCTCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGGCTCTCTCTCTGCTT**G**AGCTTGCTTGGCTGGGGACAGTGCTGCGTATCAGAGGACCTCTCTCTATGGAGATGATGT	5433
	ACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGCACTGTCCCCAGCCAAGCAAGCT**C**AAGCAGAGAGAGAGCCTTCAAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGATGTTCAA	5434
	CTCTGCTT**G**AGCTTGCT	5435
	AGCAAGCT**C**AAGCAGAG	5436
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Cys34Term TGC-TGA	TCTCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGGCTCTCTCTCTGCTTCAGCTTG**A**TTGGCTGGGGACAGTGCTGCGTATCAGAGGACCTCTCTCTATGGAGATGATGTAGTCATT	5437
	AATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGCACTGTCCCCAGCCAA**T**CAAGCTGAAGCAGAGAGAGAGCCTTCAAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5438
	TCAGCTTG**A**TTGGCTGG	5439
	CCAGCCAA**T**CAAGCTGA	5440
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Leu35Term TTG-TAG	TCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGGCTCTCTCTCTGCTTCAGCTTGCT**A**GGCTGGGGACAGTGCTGCGTATCAGAGGACCTCTCTCTATGGAGATGATGTAGTCATTGT	5441
	ACAATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGCACTGTCCCCAGCC**T**AGCAAGCTGAAGCAGAGAGAGAGCCTTCAAAGCTGTGAGAGGAAGAAGAAGAAGGACGGA	5442
	AGCTTGCT**A**GGCTGGGG	5443
	CCCCAGCC**T**AGCAAGCT	5444

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Tyr42Term TAT-TAG	TCACAGCTTTGAAGGCTCTCTCTCTGCTTCAGCTTGCTTGGCTGG GGACAGTGCTGCGTA**G**CAGAGGACCTCTCTCTATGGAGATGATGT AGTCATTGTTGCGGCACATAGGACTGCACTA	5445
	TAGTGCAGTCCTATGTGCCGCAACAATGACTACATCATCTCCATA GAGAGAGGTCCTCTG**C**TACGCAGCACTGTCCCCAGCCAAGCAAG CTGAAGCAGAGAGAGAGCCTTCAAAGCTGTGA	5446
	GCTGCGTA**G**CAGAGGAC	5447
	GTCCTCTG**C**TACGCAGC	5448
2,4-DB resistance 3-ketoacyl-CoA thiolase B *Mangifera indica* Tyr25Term TAC-TAG	CAACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTC TTCTTCTCACAATTA**G**GAGTCCGCTCTTGCCGCATCAGTATGTGCT GCAGGGGATAGCGCCGCATATCATAGGGCT	5449
	AGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATGC GGCAAGAGCGGACTC**C**TAATTGTGAGAAGAAGAATTAGAAGGGC GGAGATGCTGGAGCAACACTTGCTGTCTGTTG	5450
	CACAATTA**G**GAGTCCGC	5451
	GCGGACTC**C**TAATTGTG	5452
2,4-DB resistance 3-ketoacyl-CoA thiolase B *Magnifera indica* Glu26Term GAG-TAG	AACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTCTT CTTCTCACAATTAC**T**AGTCCGCTCTTGCCGCATCAGTATGTGCTG CAGGGGATAGCGCCGCATATCATAGGGCTT	5453
	AAGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATG CGGCAAGAGCGGACT**A**GTAATTGTGAGAAGAAGAATTAGAAGGG CGGAGATGCTGGAGCAACACTTGCTGTCTGTT	5454
	ACAATTAC**T**AGTCCGCT	5455
	AGCGGACT**A**GTAATTGT	5456
2,4-DB resistance 3-ketoacy\ol-CoA thiolase B *Mangifera indica* Ser32Term TCA-TGA	TCCAGCATCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTC CGCTCTTGCCGCAT**G**AGTATGTGCTGCAGGGGATAGCGCCGCAT ATCATAGGGCTTCTGTTTATGGAGACGATGT	5457
	ACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGCGCTATCC CCTGCAGCACATACT**C**ATGCGGCAAGAGCGGACTCGTAATTGTGA GAAGAAGAATTAGAAGGGCGGAGATGCTGGA	5458
	TGCCGCAT**G**AGTATGTG	5459
	CACATACT**C**ATGCGGCA	5460

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase B *Mangifera indica* Cys34Term TGT-TGA	TCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTCCGCTCTT GCCGCATCAGTATG**A**GCTGCAGGGGATAGCGCCGCATATCATAG GGCTTCTGTTTATGGAGACGATGTGGTGATT	5461
	AATCACCACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGC GCTATCCCCTGCAGC**T**CATACTGATGCGGCAAGAGCGGACTCGT AATTGTGAGAAGAAGAATTAGAAGGGCGGAGA	5462
	TCAGTATG**A**GCTGCAGG	5463
	CCTGCAGC**T**CATACTGA	5464
2,4-DB resistance 3-ketoacyl-CoA thiolase B *Mangifera indica* Tyr42Term TAT-TAG	TCACAATTACGAGTCCGCTCTTGCCGCATCAGTATGTGCTGCAGG GGATAGCGCCGCATA**G**CATAGGGCTTCTGTTTATGGAGACGATGT GGTGATTGTGGCAGCTCATCGTACTGCACTT	5465
	AAGTGCAGTACGATGAGCTGCCACAATCACCACATCGTCTCCATA AACAGAAGCCCTATG**C**TATGCGGCGCTATCCCCTGCAGCACATAC TGATGCGGCAAGAGCGGACTCGTAATTGTGA	5466
	GCCGCATA**G**CATAGGGC	5467
	GCCCTATG**C**TATGCGGC	5468
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Tyr22Term TAC-TAG	GAAGGCGATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCC TTCTTCTTCCGCTTA**G**ACAAATGAATCTTCGCTCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCTTCGTATCAA	5469
	TTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCATTTGT**C**TAAGCGGAAGAAGAAGGCCGGAGATGATG TAGCAAAATGCTCTGCCTGTTGATCGCCTTC	5470
	TCCGCTTA**G**ACAAATGA	5471
	TCATTTGT**C**TAAGCGGA	5472
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTT CCGCTTACACAAAT**T**AATCTTCGCTCTCTGCATCGGTTTGTGCAGC TGGGGATAGTGCTTCGTATCAAAGGACAT	5473
	ATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATT**A**ATTTGTGTAAGCGGAAGAAGAAGGCCGG AGATGATGTAGCAAAATGCTCTGCCTGTTGAT	5474
	ACACAAAT**T**AATCTTCG	5475
	CGAAGATT**A**ATTTGTGT	5476

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Ser27Term TCG-TAG	GGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTTCCGCTTA CACAAATGAATCTT**A**GCTCTCTGCATCGGTTTGTGCAGCTGGGGA TAGTGCTTCGTATCAAAGGACATCGGTGTT	5477
	AACACCGATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGC**T**AAGATTCATTTGTGTAAGCGGAAGAAGAA GGCCGGAGATGATGTAGCAAAATGCTCTGCC	5478
	TGAATCTT**A**GCTCTCTG	5479
	CAGAGAGC**T**AAGATTCA	5480
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATC TTCGCTCTCTGCAT**A**GGTTTGTGCAGCTGGGGATAGTGCTTCGTA TCAAAGGACATCGGTGTTTGGAGATGATGT	5481
	ACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCACTATCCC CAGCTGCACAAACC**T**ATGCAGAGAGCGAAGATTCATTTGTGTAAG CGGAAGAAGAAGGCCGGAGATGATGTAGCA	5482
	CTCTGCAT**A**GGTTTGTG	5483
	CACAAACC**T**ATGCAGAG	5484
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Cys33Term TGT-TGA	TCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATCTTCGCTC TCTGCATCGGTTTG**A**GCAGCTGGGGATAGTGCTTCGTATCAAAGG ACATCGGTGTTTGGAGATGATGTCGTGATT	5485
	AATCACGACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCA CTATCCCCAGCTGC**T**CAAACCGATGCAGAGAGCGAAGATTCATTT GTGTAAGCGGAAGAAGAAGGCCGGAGATGA	5486
	TCGGTTTG**A**GCAGCTGG	5487
	CCAGCTGC**T**CAAACCGA	5488
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Tyr22Term TAT-TAG	GAAGGCAATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCC TTCATCTTCGGCTTA**G**AGCCATGAATCTTCGCTCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCGTCGTATCAA	5489
	TTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCATGGCT**C**TAAGCCGAAGATGAAGGCCGGAGATGAT GTAGCAGAATGCTCTGCCTGTTGATTGCCTTC	5490
	TCGGCTTA**G**AGCCATGA	5491
	TCATGGCT**C**TAAGCCGA	5492

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATTAATCTTCGCTCTCTGCATCGGTTTGTGCAGCTGGGGATAGTGCGTCGTATCAAAGAACGT	5493
	ACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAGCGAAGATTAATGGCTATAAGCCGAAGATGAAGGCCGGAGATGATGTAGCAGAATGCTCTGCCTGTTGAT	5494
	ATAGCCATTAATCTTCG	5495
	CGAAGATTAATGGCTAT	5496
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Ser27Term TCG-TAG	GGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTAGCTCTCTGCATCGGTTTGTGCAGCTGGGGATAGTGCGTCGTATCAAAGAACGTCGGTGTT	5497
	AACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAGCTAAGATTCATGGCTATAAGCCGAAGATGAAGGCCGGAGATGATGTAGCAGAATGCTCTGCC	5498
	TGAATCTTAGCTCTCTG	5499
	CAGAGAGCTAAGATTCA	5500
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTCGCTCTCTGCATAGGTTTGTGCAGCTGGGGATAGTGCGTCGTATCAAAGAACGTCGGTGTTTGGAGATGATGT	5501
	ACATCATCTCCAAACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCTATGCAGAGAGCGAAGATTCATGGCTATAAGCCGAAGATGAAGGCCGGAGATGATGTAGCA	5502
	CTCTGCATAGGTTTGTG	5503
	CACAAACCTATGCAGAG	5504
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Cys33Term TGT-TGA	TCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTCGCTCTCTGCATCGGTTTGAGCAGCTGGGGATAGTGCGTCGTATCAAAGAACGTCGGTGTTTGGAGATGATGTCGTGATA	5505
	TATCACGACATCATCTCCAAACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCATGGCTATAAGCCGAAGATGAAGGCCGGAGATGA	5506
	TCGGTTTGAGCAGCTGG	5507
	CCAGCTGCTCAAACCGA	5508
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln5Term CAG-TAG	TCATAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTATGGCAACTCATTAGCAAACGCAACCTCCTTCCGATTTTCCCGCTCTTGCCGATGAAAATTCCCAGATTCCAG	5509
	CTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGGAAGGAGGTTGCGTTTGCTAATGAGTTGCCATAGCAGCTCACTAACCTTGGAAGAATCCAAGCGGCAAAAGAGACTATGA	5510

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAACTCAT**T**AGCAAACG	5511
	CGTTTGCT**A**ATGAGTTG	5512
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln6Term CAA-TAA	TAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTA TGGCAACTCATCAG**T**AAACGCAACCTCCTTCCGATTTTCCCGCTC TTGCCGATGAAAATTCCCAGATTCCAGGTT	5513
	AACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGG AAGGAGGTTGCGTTT**A**CTGATGAGTTGCCATAGCAGCTCACTAAC CTTGGAAGAATCCAAGCGGCAAAAGAGACTA	5514
	CTCATCAG**T**AAACGCAA	5515
	TTGCGTTT**A**CTGATGAG	5516
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln8Term CAA-TAA	CTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTATGGCA ACTCATCAGCAAACG**T**AACCTCCTTCCGATTTTCCCGCTCTTGCC GATGAAAATTCCCAGATTCCAGGTTCAATTT	5517
	AAATTGAACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAA AATCGGAAGGAGGTT**A**CGTTTGCTGATGAGTTGCCATAGCAGCTC ACTAACCTTGGAAGAATCCAAGCGGCAAAAG	5518
	AGCAAACG**T**AACCTCCT	5519
	AGGAGGTT**A**CGTTTGCT	5520
2,4 DB resistance Pex14 *Arabidopsis thaliana* Glu19Term GAA-TAA	GCTGCTATGGCAACTCATCAGCAAACGCAACCTCCTTCCGATTTT CCCGCTCTTGCCGAT**T**AAAATTCCCAGATTCCAGGTTCAATTTACA CCTTCTAATCATTATTTCTTAATTTTTCTT	5521
	AAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAATTGAACCTGG AATCTGGGAATTTT**A**ATCGGCAAGAGCGGGAAAATCGGAAGGAG GTTGCGTTTGCTGATGAGTTGCCATAGCAGC	5522
	TTGCCGAT**T**AAAATTCC	5523
	GGAATTTT**A**ATCGGCAA	5524
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln22Term CAG-TAG	GCAACTCATCAGCAAACGCAACCTCCTTCCGATTTTCCCGCTCTT GCCGATGAAAATTCC**T**AGATTCCAGGTTCAATTTACACCTTCTAAT CATTATTTCTTAATTTTTCTTTGGTGGATT	5525
	AATCCACCAAAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAATT GAACCTGGAATCT**A**GGAATTTTCATCGGCAAGAGCGGGAAAATCG GAAGGAGGTTGCGTTTGCTGATGAGTTGC	5526
	AAAATTCC**T**AGATTCCA	5527
	TGGAATCT**A**GGAATTTT	5528

Example 8

Production of albino mutants for the analysis of photosynthetic processes

Plant productivity is limited by resources available and the ability of plants to harness these resources. The conversion of light to chemical energy, which is then used to synthesize carbohydrates, fatty acids, sugars, amino acids and other compounds, requires a complex system which combines the light harvesting apparatus of pigments and proteins. The value of light energy to the plant can only be realized when it is efficiently converted into chemical energy by photosynthesis and fed into various biochemical processes. Significant effort has therefore been directed at studying photosynthetic processes in plants in order to improve productivity and/or the efficiency of photosynthesis. The analysis of the photosynthetic process is substantially aided by the ability to produce albino plants.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 18
Oligonucleotides to produce albino plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
White leaves Immutans *Arabidopsis thaliana* Ser5Term TCA-TGA	TTCTTTCCTGTGAAATTATCTGCTCAAATCTTTGGTTCCTGACGGAGATGGCGGCGATTT**G**AGGCATCTCCTCTGGTACGTTGACGATTTCACGGCCTTTGGTTACTCTTCGACGCTCTAG	5529
	CTAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTACCAGAGGAGATGCCT**C**AAATCGCCGCCATCTCCGTCAGGAACCAAAGATTTGAGCAGATAATTTCACAGGAAAGAA	5530
	GGCGATTT**G**AGGCATCT	5531
	AGATGCCT**C**AAATCGCC	5532
White leaves Immutans *Arabidopsis thaliana* Leu12Term TTG-TAG	GCTCAAATCTTTGGTTCCTGACGGAGATGGCGGCGATTTCAGGCATCTCCTCTGGTACGT**A**GACGATTTCACGGCCTTTGGTTACTCTTCGACGCTCTAGAGCCGCCGTTTCGTACAGCTC	5533
	GAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTC**T**ACGTACCAGAGGAGATGCCTGAAATCGCCGCCATCTCCGTCAGGAACCAAAGATTTGAGC	5534
	TGGTACGT**A**GACGATTT	5535
	AAATCGTC**T**ACGTACCA	5536
White leaves Immutans *Arabidopsis thaliana* Ser15Term TCA-TGA	TTTGGTTCCTGACGGAGATGGCGGCGATTTCAGGCATCTCCTCTGGTACGTTGACGATTT**G**ACGGCCTTTGGTTACTCTTCGACGCTCTAGAGCCGCCGTTTCGTACAGCTCCTCTCACCG	5537
	CGGTGAGAGGAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAGAGTAACCAAAGGCCGT**C**AAATCGTCAACGTACCAGAGGAGATGCCTGAAATCGCCGCCATCTCCGTCAGGAACCAAA	5538
	GACGATTT**G**ACGGCCTT	5539
	AAGGCCGT**C**AAATCGTC	5540
White leaves Immutans *Arabidopsis thaliana* Arg22Term CGA-TGA	GCGGCGATTTCAGGCATCTCCTCTGGTACGTTGACGATTTCACGGCCTTTGGTTACTCTT**T**GACGCTCTAGAGCCGCCGTTTCGTACAGCTCCTCTCACCGATTGCTTCATCATCTTCCTC	5541
	GAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTGTACGAAACGGCGGCTCTAGAGCGTC**A**AAGAGTAACCAAAGGCCGTGAAATCGTCAACGTACCAGAGGAGATGCCTGAAATCGCCGC	5542
	TTACTCTT**T**GACGCTCT	5543
	AGAGCGTC**A**AAGAGTAA	5544

White leaves Immutans *Arabidopsis thaliana* Arg25Term AGA-TGA	TCAGGCATCTCCTCTGGTACGTTGACGATTTCACGGCCTTTGGTTA CTCTTCGACGCTCT**T**GAGCCGCCGTTTCGTACAGCTCCTCTCACC GATTGCTTCATCATCTTCCTCTCTCTTCTC	5545
	GAGAAGAGAGAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTG TACGAAACGGCGGCTC**A**AGAGCGTCGAAGAGTAACCAAAGGCCG TGAAATCGTCAACGTACCAGAGGAGATGCCTGA	5546
	GACGCTCT**T**GAGCCGCC	5547
	GGCGGCTC**A**AGAGCGTC	5548
White leaves Immutans *Lycopersicon esculentum* Gly11Term GGA-TGA	GATTCTTGTGGGAAGGAAGAAGGATCAAGAATGGCGATTTCGATTT CTGCTATGAGTTTT**T**GAACCTCAGTTTCTTCATATTCTTGTTTTAGA GCTAGGAGTTTTGAGAAGTCATCAGTTT	5549
	AAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGAATATGAA GAAACTGAGGTTC**A**AAAACTCATAGCAGAAATCGAAATCGCCATTC TTGATCCTTCTTCCTTCCCACAAGAATC	5550
	TGAGTTTT**T**GAACCTCA	5551
	TGAGGTTC**A**AAAACTCA	5552
White leaves Immutans *Lycopersicon esculentum* Ser13Term TCA-TGA	GTGGGAAGGAAGAAGGATCAAGAATGGCGATTTCGATTTCTGCTA TGAGTTTTGGAACCT**G**AGTTTCTTCATATTCTTGTTTTAGAGCTAGG AGTTTTGAGAAGTCATCAGTTTTATGCAA	5553
	TTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGA ATATGAAGAAACT**C**AGGTTCCAAAACTCATAGCAGAAATCGAAATC GCCATTCTTGATCCTTCTTCCTTCCCAC	5554
	TGGAACCT**G**AGTTTCTT	5555
	AAGAAACT**C**AGGTTCCA	5556
White leaves Immutans *Lycopersicon esculentum* Ser16Term TCA-TGA	AAGAAGGATCAAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGG AACCTCAGTTTCTT**G**ATATTCTTGTTTTAGAGCTAGGAGTTTTGAGA AGTCATCAGTTTTATGCAATTCCCAGAA	5557
	TTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTC TAAAACAAGAATAT**C**AAGAAACTGAGGTTCCAAAACTCATAGCAGA AATCGAAATCGCCATTCTTGATCCTTCTT	5558
	AGTTTCTT**G**ATATTCTT	5559
	AAGAATAT**C**AAGAAACT	5560
White leaves Immutans *Lycopersicon esculentum* Tyr17Term TAT-TAG	AGGATCAAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGGAACC TCAGTTTCTTCATA**G**TCTTGTTTTAGAGCTAGGAGTTTTGAGAAGTC ATCAGTTTTATGCAATTCCCAGAACCCA	5561
	TGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTA GCTCTAAAACAAGA**C**TATGAAGAAACTGAGGTTCCAAAACTCATAG CAGAAATCGAAATCGCCATTCTTGATCCT	5562
	TCTTCATA**G**TCTTGTTT	5563
	AAACAAGA**C**TATGAAGA	5564

White leaves Immutans *Lycopersicon esculentum* Cys19Term TGT-TGA	AAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGGAACCTCAGTTTCTTCATATTCTTG**A**TTTAGAGCTAGGAGTTTTGAGAAGTCATCAGTTTTATGCAATTCCCAGAACCCATGTCGG	5565
	CCGACATGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAA**T**CAAGAATATGAAGAAACTGAGGTTCCAAAACTCATAGCAGAAATCGAAATCGCCATTCTT	5566
	TATTCTTG**A**TTTAGAGC	5567
	GCTCTAAA**T**CAAGAATA	5568
White leaves Immutans *Capsicum annuum* Ser13Term TCA-TGA	CGCGTCCGATAAAAAAATCAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAACTT**G**AGTTTCTTCTTCATATTCAGCATTTTTGTGCAATTCCAAGAACCCATTTTGTTTGAATTC	5569
	GAATTCAAACAAAATGGGTTCTTGGAATTGCACAAAAATGCTGAATATGAAGAAGAAACT**C**AAGTTCGAAAACTCATAGCAGATATGGAAATCGCCATTCTTGATTTTTTTATCGGACGCG	5570
	TCGAACTT**G**AGTTTCTT	5571
	AAGAAACT**C**AAGTTCGA	5572
White leaves Immutans *Capsicum annuum* Ser17Term TCA-TGA	AAAAATCAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTT**G**ATATTCAGCATTTTTGTGCAATTCCAAGAACCCATTTTGTTTGAATTCTCTATTTTCACT	5573
	AGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAATTGCACAAAAATGCTGAATAT**C**AAGAAGAAACTGAAGTTCGAAAACTCATAGCAGATATGGAAATCGCCATTCTTGATTTTT	5574
	TTCTTCTT**G**ATATTCAG	5575
	CTGAATAT**C**AAGAAGAA	5576
White leaves Immutans *Capsicum annuum* Ser19Term TCA-TGA	CAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCATATT**G**AGCATTTTTGTGCAATTCCAAGAACCCATTTTGTTTGAATTCTCTATTTTCACTTAGGAA	5577
	TTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAATTGCACAAAAATGCT**C**AATATGAAGAAGAAACTGAAGTTCGAAAACTCATAGCAGATATGGAAATCGCCATTCTTG	5578
	TTCATATT**G**AGCATTTT	5579
	AAAATGCT**C**AATATGAA	5580
White leaves Immutans *Capsicum annuum* Leu21Term TTG-TAG	CGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCATATTCAGCATTTT**A**GTGCAATTCCAAGAACCCATTTTGTTTGAATTCTCTATTTTCACTTAGGAATTCTCATAG	5581
	CTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAATTGCAC**T**AAAATGCTGAATATGAAGAAGAAACTGAAGTTCGAAAACTCATAGCAGATATGGAAATCG	5582
	AGCATTTT**A**GTGCAATT	5583
	AATTGCAC**T**AAAATGCT	5584

White leaves Immutans *Capsicum annuum* Cys22Term TGC-TGA	TTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCATATTCAGCATTTTTGTG**A**AATTCCAAGAACCCATTTTGTTTGAATTCTCTATTTTCACTTAGGAATTCTCATAGAACT	5585
	AGTTCTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAATT**T**CACAAAAATGCTGAATATGAAGAAGAAACTGAAGTTCGAAAACTCATAGCAGATATGGAA	5586
	TTTTTGTG**A**AATTCCAA	5587
	TTGGAATT**T**CACAAAAA	5588
White leaves Immutans *Oryza sativa* Glu22Term GAG-TAG	TTCGGCACGAGGGAGAAGGAGCAGACCGAGGTGGCCGTCGAGGAGTCCTTCCCCTTCAGG**T**AGACGGCTCCTCCTGACGAGCCACTGGTCACCGCCGAGGAGAGCTGGGTGGTTAAGCTCG	5589
	CGAGCTTAACCACCCAGCTCTCCTCGGCGGTGACCAGTGGCTCGTCAGGAGGAGCCGTCT**A**CCTGAAGGGGAAGGACTCCTCGACGGCCACCTCGGTCTGCTCCTTCTCCCTCGTGCCGAA	5590
	CCTTCAGG**T**AGACGGCT	5591
	AGCCGTCT**A**CCTGAAGG	5592
White leaves Immutans *Oryza sativa* Glu28Term CAG-TAG	GAGCAGACCGAGGTGGCCGTCGAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGAC**T**AGCCACTGGTCACCGCCGAGGAGAGCTGGGTGGTTAAGCTCGAGCAGTCCGTGAACATTT	5593
	AAATGTTCACGGACTGCTCGAGCTTAACCACCCAGCTCTCCTCGGCGGTGACCAGTGGCT**A**GTCAGGAGGAGCCGTCTCCCTGAAGGGGAAGGACTCCTCGACGGCCACCTCGGTCTGCTC	5594
	CTCCTGAC**T**AGCCACTG	5595
	CAGTGGCT**A**GTCAGGAG	5596
White leaves Immutans *Oryza sativa* Glu34Term GAG-TAG	GTCGAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCACCGCC**T**AGGAGAGCTGGGTGGTTAAGCTCGAGCAGTCCGTGAACATTTTCCTCACGGAGTCAGTCA	5597
	TGACTGACTCCGTGAGGAAAATGTTCACGGACTGCTCGAGCTTAACCACCCAGCTCTCCT**A**GGCGGTGACCAGTGGCTCGTCAGGAGGAGCCGTCTCCCTGAAGGGGAAGGACTCCTCGAC	5598
	TCACCGCC**T**AGGAGAGC	5599
	GCTCTCCT**A**GGCGGTGA	5600
White leaves Immutans *Oryza sativa* Glu35Term GAG-TAG	GAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCACCGCCGAG**T**AGAGCTGGGTGGTTAAGCTCGAGCAGTCCGTGAACATTTTCCTCACGGAGTCAGTCATCA	5601
	TGATGACTGACTCCGTGAGGAAAATGTTCACGGACTGCTCGAGCTTAACCACCCAGCTCT**A**CTCGGCGGTGACCAGTGGCTCGTCAGGAGGAGCCGTCTCCCTGAAGGGGAAGGACTCCTC	5602
	CCGCCGAG**T**AGAGCTGG	5603
	CCAGCTCT**A**CTCGGCGG	5604

White leaves Immutans *Oryza sativa* Trp37Term TGG-TGA	CTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCACCGCCGAGGAGAGCTG**A**GTGGTTAAGCTCGAGCAGTCCGTGAACATTTTCCTCACGGAGTCAGTCATCACGATACTT	5605
	AAGTATCGTGATGACTGACTCCGTGAGGAAAATGTTCACGGACTGCTCGAGCTTAACCAC**T**CAGCTCTCCTCGGCGGTGACCAGTGGCTCGTCAGGAGGAGCCGTCTCCCTGAAGGGGAAG	5606
	GAGAGCTG**A**GTGGTTAA	5607
	TTAACCAC**T**CAGCTCTC	5608
White leaves Immutans *Triticum aestivum* Trp22Term TGG-TGA	TCCGGAGGAGGAAGGGGGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTG**A**GTCGTCAGATTCGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATACTC	5609
	GAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTGCTCGAATCTGACGAC**T**CAGTCGCCGTCCTCGCCGGCGAGGGTGAGCTCCTCGTCGAATCCCCCTTCCTCCTCCGGA	5610
	GGCGACTG**A**GTCGTCAG	5611
	CTGACGAC**T**CAGTCGCC	5612
White leaves Immutans *Triticum aestivum* Arg25Term AGA-TGA	GAGGAAGGGGGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTGGGTCGTC**T**GATTCGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATACTCGATATTC	5613
	GAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTGCTCGAATC**A**GACGACCCAGTCGCCGTCCTCGCCGGCGAGGGTGAGCTCCTCGTCGAATCCCCCTTCCTC	5614
	GGGTCGTC**T**GATTCGAG	5615
	CTCGAATC**A**GACGACCC	5616
White leaves Immutans *Triticum aestivum* Glu27Term GAG-TAG	GGGGGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTGGGTCGTCAGATTC**T**AGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATACTCGATATTCTGTATC	5617
	GATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTGCT**A**GAATCTGACGACCCAGTCGCCGTCCTCGCCGGCGAGGGTGAGCTCCTCGTCGAATCCCCC	5618
	TCAGATTC**T**AGCAGTCC	5619
	GGACTGCT**A**GAATCTGA	5620
White leaves Immutans *Triticum aestivum* Gln28Term CAG-TAG	GGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTGGGTCGTCAGATTCGAG**T**AGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATACTCGATATTCTGTATCGTG	5621
	CACGATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACT**A**CTCGAATCTGACGACCCAGTCGCCGTCCTCGCCGGCGAGGGTGAGCTCCTCGTCGAATCC	5622
	GATTCGAG**T**AGTCCTTC	5623
	GAAGGACT**A**CTCGAATC	5624

White leaves Immutans *Triticum aestivum* Tyr46Term TAT-TAG	CGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATA CTCGATATTCTGTA**G**CGTGACCGCGACTACGCAAGGTTCTTCGTG CTCGAGACCATCGCCAGGGTGCCCTATTTC	5625
	GAAATAGGGCACCCTGGCGATGGTCTCGAGCACGAAGAACCTTG CGTAGTCGCGGTCACG**C**TACAGAATATCGAGTATAAAGATGACAG TATCCGTGAGGAATACGTTGAAGGACTGCTCG	5626
	ATTCTGTA**G**CGTGACCG	5627
	CGGTCACG**C**TACAGAAT	5628

Example 9

Altering amino acid content of plants

Another aim of biotechnology is to generate plants, especially crop plants, with added value traits. An example of such a trait is improved nutritional quality in food crops. For example, lysine, tryptophan and threonine, which are essential amino acids in the diet of humans and many animals, are limiting nutrients in most cereal crops. Consequently, grain-based diets, such as those based on corn, barley, wheat, rice, maize, millet, sorghum, and the like, must be supplemented with more expensive synthetic amino acids or amino-acid-containing oilseed protein meals. Increasing the lysine content of these grains or of any of the feed component crops would result in significant added value.

Naturally occurring mutants of plants that have different levels of particular essential amino acids have been identified. However, these mutants are generally not the result of increased free amino acid, but are instead the result of shifts in the overall protein profile of the grain. For example, in maize, reduced levels of lysine-deficient endosperm proteins (prolamines) are complemented by elevated levels of more lysine-rich proteins (albumins, globulins and glutelins). While nutritionally superior, these mutants are associated with reduced yields and poor grain quality, limiting their agronomic usefulness.

An alternative approach is to generate plants with mutations that render key amino acid biosynthetic enzymes insensitive to feedback inhibition. Many such mutations are known and mutation results in increased free amino acid. The increased production can optionally be coupled to increased expression of an abundant storage protein comprising the chosen amino acid. Alternatively, a normally abundant protein can be engineered to contain more of the target amino acid.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that remove feedback inhibition in plant amino acid biosynthetic enzymes.

Table 19
Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS *Arabidopsis thaliana* Arg77His CGT-CAT	TATCCTCCAGGATCTTAAGATTTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCC**A**TAGAAACTGTAGCAACATCGGTGTTGCACAGATCGTGGCGGCTAAGTGGTCCAACAACCC	5629
	GGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACCGATGTTGCTACAGTTTCTA**T**GGGCTTTAATGCTGAGCTGACGGACGAAATTAGGAGGAAATCTTAAGATCCTGGAGGATA	5630
	TAAAGCCC**A**TAGAAACT	5631
	AGTTTCTA**T**GGGCTTTA	5632
Met Overproduction CGS *Arabidopsis thaliana* Ser81Asn AGC-AAC	TCTTAAGATTTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCGTAGAAACTGTA**A**CAACATCGGTGTTGCACAGATCGTGGCGGCTAAGTGGTCCAACAACCCATCCTCCGCGTT	5633
	AACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACCGATGTTG**T**TACAGTTTCTACGGGCTTTAATGCTCAGCTGACGGACGAAATTAGGAGGAAATCTTAAGA	5634
	AAACTGTA**A**CAACATCG	5635
	CGATGTTG**T**TACAGTTT	5636
Met Overproduction CGS *Arabidopsis thaliana* Gly84Ser GGT-AGT	TTTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCGTAGAAACTGTAGCAACATC**A**GTGTTGCACAGATCGTGGCGGCTAAGTGGTCCAACAACCCATCCTCCGCGTTACCTTCGG	5637
	CCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACAC**T**GATGTTGCTACAGTTTCTACGGGCTTTAATGCTCAGCTGACGGACGAAATTAGGAGGAAA	5638
	GCAACATC**A**GTGTTGCA	5639
	TGCAACAC**T**GATGTTGC	5640
Met Overproduction CGS *Arabidopsis thaliana* Gly84Asp GGT-GAT	TTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCGTAGAAACTGTAGCAACATCG**A**TGTTGCACAGATCGTGGCGGCTAAGTGGTCCAACAACCCATCCTCCGCGTTACCTTCGGC	5641
	GCCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACA**T**CGATGTTGCTACAGTTTCTACGGGCTTTAATGCTCAGCTGACGGACGAAATTAGGAGGAA	5642
	CAACATCG**A**TGTTGCAC	5643
	GTGCAACA**T**CGATGTTG	5644

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS *Fragraria vesca* Arg73His CGC-CAC	TATCGTCACTCATCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCC**A**CCGCAACTGCAGCAACATCGGCGTCGCGCAGATCGTCGCGGCTTCGTGGTCCAACAAAGA	5645
	TCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGCCGATGTTGCTGCAGTTGCGG**T**GGGCCTTGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAAGCGGAGGATGAGTGACGATA	5646
	CAAGGCCC**A**CCGCAACT	5647
	AGTTGCGG**T**GGGCCTTG	5648
Met Overproduction CGS *Fragraria vesca* Ser77Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCGCAACTGCA**A**CAACATCGGCGTCGCGCAGATCGTCGCGGCTTCGTGGTCCAACAAAGACTCCGACCTTTC	5649
	GAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGCCGATGTTG**T**TGCAGTTGCGGCGGGCCTTGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAAGCGGAGGA	5650
	CAACTGCA**A**CAACATCG	5651
	CGATGTTG**T**TGCAGTTG	5652
Met Overproduction CGS *Fragraria vesca* Gly80Ser GGC-AGC	TTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCGCAACTGCAGCAACATC**A**GCGTCGCGCAGATCGTCGCGGCTTCGTGGTCCAACAAAGACTCCGACCTTTCGGCGGTGC	5653
	GCACCGCCGAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGC**T**GATGTTGCTGCAGTTGCGGCGGGCCTTGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAA	5654
	GCAACATC**A**GCGTCGCG	5655
	CGCGACGC**T**GATGTTGC	5656
Met Overproduction CGS *Fragraria vesca* Gly80Asp GGC-GAC	TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCGCAACTGCAGCAACATCG**A**CGTCGCGCAGATCGTCGCGGCTTCGTGGTCCAACAAAGACTCCGACCTTTCGGCGGTGCC	5657
	GGCACCGCCGAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACG**T**CGATGTTGCTGCAGTTGCGGCGGGCCTTGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGA	5658
	CAACATCG**A**CGTCGCGC	5659
	GCGCGACG**T**CGATGTTG	5660
Met Overproduction CGS *Glycine max* Arg68His CGC-CAC	TCTCCTCCCTCATCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCG**A**GCCGCAACTGCAGCAACATCGGCGTCGCGCAAATCGTCGCCGCTTCGTGGTCGAACAACAG	5661
	CTGTTGTTCGACCACGAAGCGGCGACGATTTGCGCGACGCCGATGTTGCTGCAGTTGCGGC**T**CGCCTTGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAAGCGGAGGATGAGGGAGGAGA	5662
	CCAAGGCG**A**GCCGCAAC	5663

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTGCGGCTCGCCTTGG	5664
Met Overproduction CGS *Glycine max* Ser72Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAG GCGCGCCGCAACTGCAACAACATCGGCGTCGCGCAAATCGTCGC CGCTTCGTGGTCGAACAACAGCGACAACTCTCC	5665
	GGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGCGACGATTTG CGCGACGCCGATGTTGTTGCAGTTGCGGCGCGCCTTGGTGCTTA GCTGGCGCTGGAAGTTGGGAGGGAAGCGGAGGA	5666
	CAACTGCAACAACATCG	5667
	CGATGTTGTTGCAGTTG	5668
Met Overproduction CGS *Glycine max* Gly75Ser GGC-AGC	TTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCG CAACTGCAGCAACATCAGCGTCGCGCAAATCGTCGCCGCTTCGT GGTCGAACAACAGCGACAACTCTCCGGCCGCCG	5669
	CGGCGGCCGGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGC GACGATTTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGCGCCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA	5670
	GCAACATCAGCGTCGCG	5671
	CGCGACGCTGATGTTGC	5672
Met Overproduction CGS *Glycine max* Gly75Asp GGC-GAC	TCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCGC AACTGCAGCAACATCGACGTCGCGCAAATCGTCGCCGCTTCGTG GTCGAACAACAGCGACAACTCTCCGGCCGCCGG	5673
	CCGGCGGCCGGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGC GACGATTTGCGCGACGTCGATGTTGCTGCAGTTGCGGCGCGCCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGA	5674
	CAACATCGACGTCGCGC	5675
	GCGCGACGTCGATGTTG	5676
Met Overproduction CGS *Solanum tuberosum* Arg70His AGG-CAC	TGTCTTCTCTGATTTTCAGGTTTCCTCCTAATTTCGTGAGGCAGCT AAGCATTAAGGCT**CAC**AGGAATTGCAGCAATATTGGCGTGGCTCA AGTTGTGGCGGCTTCCTGGTCTAACAACCA	5677
	TGGTTGTTAGACCAGGAAGCCGCCACAACTTGAGCCACGCCAATA TTGCTGCAATTCCT**GTG**AGCCTTAATGCTTAGCTGCCTCACGAAAT TAGGAGGAAACCTGAAAATCAGAGAAGACA	5678
	TAAGGCT**CAC**AGGAATT	5679
	AATTCCT**GTG**AGCCTTA	5680
Met Overproduction CGS *Solanum tuberosum* Ser74Asn AGC-AAC	TTTTCAGGTTTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGC TAGGAGGAATTGCAACAATATTGGCGTGGCTCAAGTTGTGGCGG CTTCCTGGTCTAACAACCAAGCCGGTCCTGA	5681
	TCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCCACAACTTG AGCCACGCCAATATTGTTGCAATTCCTCCTAGCCTTAATGCTTAGC TGCCTCACGAAATTAGGAGGAAACCTGAAAA	5682

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAATTGCA**A**CAATATTG	5683
	CAATATTG**T**TGCAATTC	5684
Met Overproduction CGS *Solanum tuberosum* Gly77Ser GGC-AGC	TTTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGCTAGGAGG AATTGCAGCAATATT**A**GCGTGGCTCAAGTTGTGGCGGCTTCCTGG TCTAACAACCAAGCCGGTCCTGAATTCACTC	5685
	GAGTGAATTCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCC ACAACTTGAGCCACGC**T**AATATTGCTGCAATTCCTCCTAGCCTTAA TGCTTAGCTGCCTCACGAAATTAGGAGGAAA	5686
	GCAATATT**A**GCGTGGCT	5687
	AGCCACGC**T**AATATTGC	5688
Met Overproduction CGS *Solanum tuberosum* Gly77Asp GGC-GAC	TTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGCTAGGAGGA ATTGCAGCAATATTG**A**CGTGGCTCAAGTTGTGGCGGCTTCCTGGT CTAACAACCAAGCCGGTCCTGAATTCACTCC	5689
	GGAGTGAATTCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGC CACAACTTGAGCCACG**T**CAATATTGCTGCAATTCCTCCTAGCCTTA ATGCTTAGCTGCCTCACGAAATTAGGAGGAA	5690
	CAATATTG**A**CGTGGCTC	5691
	GAGCCACG**T**CAATATTG	5692
Met Overproduction CGS *Mesembryanthemum crystallinum* Arg73His CGC-CAC	CTTCCTCTCTTATCCTTCGCTTTCCTCCCAACTTTGTCCGTCAGCT CAGCACCAAGGCTCGCC**A**CAACTGCAGCAACATTGGTGTCGCAC AGGTCGTCGCTGCCTCCTGGTCCAACAACTC	5693
	GAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACACCAAT GTTGCTGCAGTTG**T**GGCGAGCCTTGGTGCTGAGCTGACGGACAA AGTTGGGAGGAAAGCGAAGGATAAGAGAGGAAG	5694
	GGCTCGCC**A**CAACTGCA	5695
	TGCAGTTG**T**GGCGAGCC	5696
Met Overproduction CGS *Mesembryanthemum crystallinum* Ser77Asn AGC-AAC	TCCTTCGCTTTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGG CTCGCCGCAACTGCA**A**CAACATTGGTGTCGCACAGGTCGTCGCT GCCTCCTGGTCCAACAACTCCGATGCCGGCGC	5697
	GCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCT GTGCGACACCAATGTTG**T**TGCAGTTGCGGCGAGCCTTGGTGCTG AGCTGACGGACAAAGTTGGGAGGAAAGCGAAGGA	5698
	CAACTGCA**A**CAACATTG	5699
	CAATGTTG**T**TGCAGTTG	5700

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS *Mesembryanthemum crystallinum* Gly80Ser GGT-AGT	TTTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGCAACTGCAGCAACATT**A**GTGTCGCACAGGTCGTCGCTGCCTCCTGGTCCAACAACTCCGATGCCGGCGCCACCTCTT	5701
	AAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACAC**T**AATGTTGCTGCAGTTGCGGCGAGCCTTGGTGCTGAGCTGACGGACAAAGTTGGGAGGAAA	5702
	GCAACATT**A**GTGTCGCA	5703
	TGCGACAC**T**AATGTTGC	5704
Met Overproduction CGS *Mesembryanthemum crystallinum* Gly80Asp GGT-GAT	TTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGCAACTGCAGCAACATTG**A**TGTCGCACAGGTCGTCGCTGCCTCCTGGTCCAACAACTCCGATGCCGGCGCCACCTCTTG	5705
	CAAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACA**T**CAATGTTGCTGCAGTTGCGGCGAGCCTTGGTGCTGAGCTGACGGACAAAGTTGGGAGGAA	5706
	CAACATTG**A**TGTCGCAC	5707
	GTGCGACA**T**CAATGTTG	5708
Met Overproduction CGS *Zea mays* Arg41His CGC-CAC	CCTCTGCTACCATCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCAC**A**CCGCAACTGCAGCAACATCGGCGTCGCGCAGATCGTCGCCGCCGCGTGGTCCGACTGCCC	5709
	GGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGCCGATGTTGCTGCAGTTGCGG**T**GTGCCTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAAGCGGAGGATGGTAGCAGAGG	5710
	CAAGGCAC**A**CCGCAACT	5711
	AGTTGCGG**T**GTGCCTTG	5712
Met Overproduction CGS *Zea mays* Ser45Asn AGC-AAC	TCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGCAACTGCA**A**CAACATCGGCGTCGCGCAGATCGTCGCCGCCGCGTGGTCCGACTGCCCCGCCGCTCGCCC	5713
	GGGCGAGCGGCGGGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGCCGATGTTG**T**TGCAGTTGCGGCGTGCCTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAAGCGGAGGA	5714
	CAACTGCA**A**CAACATCG	5715
	CGATGTTG**T**TGCAGTTG	5716
Met Overproduction CGS *Zea mays* Gly48Ser GGC-AGC	TTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGCAACTGCAGCAACATC**A**GCGTCGCGCAGATCGTCGCCGCCGCGTGGTCCGACTGCCCCGCCGCTCGCCCCCACTTAG	5717
	CTAAGTGGGGGCGAGCGGCGGGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGC**T**GATGTTGCTGCAGTTGCGGCGTGCCTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAA	5718
	GCAACATC**A**GCGTCGCG	5719

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCGACGC**T**GATGTTGC	5720
Met Overproduction CGS *Zea mays* Gly48Asp GGC-GAC	TTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGC AACTGCAGCAACATCG**A**CGTCGCGCAGATCGTCGCCGCCGCGTG GTCCGACTGCCCCGCCGCTCGCCCCCACTTAGG	5721
	CCTAAGTGGGGGCGAGCGGCGGGGCAGTCGGACCACGCGGCG GCGACGATCTGCGCGACG**T**CGATGTTGCTGCAGTTGCGGCGTGC CTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAA	5722
	CAACATCG**A**CGTCGCGC	5723
	GCGCGACG**T**CGATGTTG	5724
Met Overproduction TS *Arabidopsis thaliana* Leu205Arg CTT-CGT	GTATGAATGATCTGTGGGTGAAACACTGTGGGATTAGTCATACAG GAAGTTTCAAGGATC**G**TGGAATGACTGTTTTGGTTAGTCAAGTTAA TCGTCTGAGAAAGATGAAACGACCTGTGGT	5725
	ACCACAGGTCGTTTCATCTTTCTCAGACGATTAACTTGACTAACCA AAACAGTCATTCCA**C**GATCCTTGAAACTTCCTGTATGACTAATCCC ACAGTGTTTCACCCACAGATCATTCATAC	5726
	CAAGGATC**G**TGGAATGA	5727
	TCATTCCA**C**GATCCTTG	5728
Met Overproduction TS *Solanum tuberosum* Leu198Arg CTT-CGT	GCATGACTGATTTGTGGGTCAAACACTGTGGGATTAGCCATACTG GTAGTTTTAAGGATC**G**TGGGATGACTGTTTTGGTGAGTCAAGTTAA TCGCTTGCGGAAAATGCATAAACCGGTTGT	5729
	ACAACCGGTTTATGCATTTTCCGCAAGCGATTAACTTGACTCACCA AAACAGTCATCCCA**C**GATCCTTAAAACTACCAGTATGGCTAATCCC ACAGTGTTTGACCCACAAATCAGTCATGC	5730
	TAAGGATC**G**TGGGATGA	5731
	TCATCCCA**C**GATCCTTA	5732
Lys Overproduction DHPS *Zea mays* Ser157Asn AGC-AAC	TCATTGGGCACACAGTGAACTGCTTTGGCTCTAGAATCAAAGTGA TAGGCAACACAGGAA**A**CAACTCAACCAGAGAAGCCGTCCACGCA ACAGAACAGGGATTTGCTGTTGGCATGCATGC	5733
	GCATGCATGCCAACAGCAAATCCCTGTTCTGTTGCGTGGACGGCT TCTCTGGTTGAGTTG**T**TTCCTGTGTTGCCTATCACTTTGATTCTAG AGCCAAAGCAGTTCACTGTGTGCCCAATGA	5734
	CACAGGAA**A**CAACTCAA	5735
	TTGAGTTG**T**TTCCTGTG	5736
Lys Overproduction DHPS *Zea mays* Ala166Val GCA-GAA	GCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACCA GAGAAGCCGTCCACG**A**AACAGAACAGGGATTTGCTGTTGGCATG CATGCGGCTCTCCACATCAATCCTTACTACGG	5737
	CCGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGC AAATCCCTGTTCTGTT**T**CGTGGACGGCTTCTCTGGTTGAGTTGCTT CCTGTGTTGCCTATCACTTTGATTCTAGAGC	5738

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGTCCACG**A**AACAGAAC	5739
	GTTCTGTT**T**CGTGGACG	5740
Lys Overproduction DHPS *Zea mays* Ala166Thr GCA-ACA	GGCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACCAGAGAAGCCGTCCAC**A**CAACAGAACAGGGATTTGCTGTTGGCATGCATGCGGCTCTCCACATCAATCCTTACTACG	5741
	CGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGCAAATCCCTGTTCTGTTG**T**GTGGACGGCTTCTCTGGTTGAGTTGCTTCCTGTGTTGCCTATCACTTTGATTCTAGAGCC	5742
	CCGTCCAC**A**CAACAGAA	5743
	TTCTGTTG**T**GTGGACGG	5744
Lys Overproduction DHPS *Oryza sativa* Ser124Asn AGT-AAT	TTATTGGGCATACAGTTAACTGCTTTGGCACTAAAATTAAAGTGGTCGGCAACACAGGAA**A**TAACTCAACAAGGGAGGCTATTCACGCAACTGAGCAGGGATTCGCTGTAGGTATGCACGC	5745
	GCGTGCATACCTACAGCGAATCCCTGCTCAGTTGCGTGAATAGCCTCCCTTGTTGAGTTA**T**TTCCTGTGTTGCCGACCACTTTAATTTTAGTGCCAAAGCAGTTAACTGTATGCCCAATAA	5746
	CACAGGAA**A**TAACTCAA	5747
	TTGAGTTA**T**TTCCTGTG	5748
Lys Overproduction DHPS *Oryza sativa* Ala133Val GCA-GTA	GCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACAAGGGAGGCTATTCACG**T**AACTGAGCAGGGATTCGCTGTAGGTATGCACGCGGCTCTCCACATCAATCCTTACTACGG	5749
	CCGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGCGAATCCCTGCTCAGTT**A**CGTGAATAGCCTCCCTTGTTGAGTTACTTCCTGTGTTGCCGACCACTTTAATTTTAGTGC	5750
	TATTCACG**T**AACTGAGC	5751
	GCTCAGTT**A**CGTGAATA	5752
Lys Overproduction DHPS *Oryza sativa* Ala133Thr GCA-ACA	GGCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACAAGGGAGGCTATTCAC**A**CAACTGAGCAGGGATTCGCTGTAGGTATGCACGCGGCTCTCCACATCAATCCTTACTACG	5753
	CGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGCGAATCCCTGCTCAGTTG**T**GTGAATAGCCTCCCTTGTTGAGTTACTTCCTGTGTTGCCGACCACTTTAATTTTAGTGCC	5754
	CTATTCAC**A**CAACTGAG	5755
	CTCAGTTG**T**GTGAATAG	5756
Lys Overproduction DHPS 1 *Triticum aestivum* Ser165Asn AGT-AAT	TCATCGGGCATACTGTTAACTGCTTTGGAGCCAACATTAAAGTGATAGGCAACACGGGAA**A**TAACTCAACCAGAGAAGCTGTTCACGCGACAGAGCAGGGATTTGCTGTTGGCATGCATGC	5757

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCATGCATGCCAACAGCAAATCCCTGCTCTGTCGCGTGAACAGCT TCTCTGGTTGAGTTATTTCCCGTGTTGCCTATCACTTTAATGTTGG CTCCAAAGCAGTTAACAGTATGCCCGATGA	5758
	CACGGGAAATAACTCAA	5759
	TTGAGTTATTTCCCGTG	5760
Lys Overproduction DHPS 1 *Triticum aestivum* Ala174Val GCG-GTG	GAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACCA GAGAAGCTGTTCACGTGACAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTTCATGTCAATCCTTACTACGG	5761
	CCGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTCACGTGAACAGCTTCTCTGGTTGAGTTACTT CCCGTGTTGCCTATCACTTTAATGTTGGCTC	5762
	TGTTCACGTGACAGAGC	5763
	GCTCTGTCACGTGAACA	5764
Lys Overproduction DHPS 1 *Triticum aestivum* Ala174Thr GCG-ACG	GGAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACC AGAGAAGCTGTTCACACGACAGAGCAGGGATTTGCTGTTGGCAT GCATGCAGCTCTTCATGTCAATCCTTACTACG	5765
	CGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTCGTGTGAACAGCTTCTCTGGTTGAGTTACTTC CCGTGTTGCCTATCACTTTAATGTTGGCTCC	5766
	CTGTTCACACGACAGAG	5767
	CTCTGTCGTGTGAACAG	5768
Lys Overproduction DHPS 2 *Triticum aestivum* Ser154Asn AGT-AAT	TCATCGGGCACACTGTTAACTGCTTTGGAACTAACATTAAAGTGAT AGGCAACACGGGAAATAACTCAACTAGAGAAGCGATTCACGCTTC AGAGCAGGGATTTGCTGTTGGCATGCATGC	5769
	GCATGCATGCCAACAGCAAATCCCTGCTCTGAAGCGTGAATCGCT TCTCTAGTTGAGTTATTTCCCGTGTTGCCTATCACTTTAATGTTAGT TCCAAAGCAGTTAACAGTGTGCCCGATGA	5770
	CACGGGAAATAACTCAA	5771
	TTGAGTTATTTCCCGTG	5772
Lys Overproduction DHPS 2 *Triticum aestivum* Ala163Val GCT-GTT	GAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACTA GAGAAGCGATTCACGTTTCAGAGCAGGGATTTGCTGTTGGCATGC ATGCAGCTCTCCATGTCAATCCTTACTATGG	5773
	CCATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGAAACGTGAATCGCTTCTCTAGTTGAGTTACTTC CCGTGTTGCCTATCACTTTAATGTTAGTTC	5774
	GATTCACGTTTCAGAGC	5775
	GCTCTGAAACGTGAATC	5776

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lys Overproduction DHPS 2 *Triticum aestivum* Ala163Thr GCT-ACT	GGAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACTAGAGAAGCGATTCAC**A**CTTCAGAGCAGGGATTTGCTGTTGGCATGCATGCAGCTCTCCATGTCAATCCTTACTATG	5777
	CATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAAATCCCTGCTCTGAAG**T**GTGAATCGCTTCTCTAGTTGAGTTACTTCCCGTGTTGCCTATCACTTTAATGTTAGTTCC	5778
	CGATTCAC**A**CTTCAGAG	5779
	CTCTGAAG**T**GTGAATCG	5780
Lys Overproduction DHPS *Coix lacryma-jobi* Ser154Asn AGT-AAT	CTCATTGGGCATACTGTGAACTGCTTTGGCTCTAGAATTAAAGTGATAGGCAACACAGGAA**A**TAACTCAACCAGAGAAGCTGTTCACGCAACAGAGCAGGGATTTGCTGTTGGCATGCATG	5781
	CATGCATGCCAACAGCAAATCCCTGCTCTGTTGCGTGAACAGCTTCTCTGGTTGAGTTA**T**TTCCTGTGTTGCCTATCACTTTAATTCTAGAGCCAAAGCAGTTCACAGTATGCCCAATGAG	5782
	CACAGGAA**A**TAACTCAA	5783
	TTGAGTTA**T**TTCCTGTG	5784
Lys Overproduction DHPS *Coix lacryma-jobi* Ala163Val GCA-GTA	GCTCTAGAATTAAAGTGATAGGCAACACAGGAAGTAACTCAACCAGAGAAGCTGTTCACG**T**AACAGAGCAGGGATTTGCTGTTGGCATGCATGCAGCTCTCCACATCAATCCTTACTATGG	5785
	CCATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAAATCCCTGCTCTGTT**A**CGTGAACAGCTTCTCTGGTTGAGTTACTTCCTGTGTTGCCTATCACTTTAATTCTAGAGC	5786
	TGTTCACG**T**AACAGAGC	5787
	GCTCTGTT**A**CGTGAACA	5788
Lys Overproduction DHPS *Coix lacryma-jobi* Ala163Thr GCA-ACA	GGCTCTAGAATTAAAGTGATAGGCAACACAGGAAGTAACTCAACCAGAGAAGCTGTTCAC**A**CAACAGAGCAGGGATTTGCTGTTGGCATGCATGCAGCTCTCCACATCAATCCTTACTATG	5789
	CATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAAATCCCTGCTCTGTTG**T**GTGAACAGCTTCTCTGGTTGAGTTACTTCCTGTGTTGCCTATCACTTTAATTCTAGAGCC	5790
	CTGTTCAC**A**CAACAGAG	5791
	CTCTGTTG**T**GTGAACAG	5792
Lys Overproduction DHPS *Nicotiana tabacum* Ser136Asn AGC-AAC	TCATTGGTCACACAGTCAATTGTTTTGGAGGGTCCATCAAAGTCATCGGGAACACTGGAA**A**CAACTCCACAAGGGAAGCAATCCATGCAACTGAACAGGGATTTGCTGTAGGTATGCATGC	5793
	GCATGCATACCTACAGCAAATCCCTGTTCAGTTGCATGGATTGCTTCCCTTGTGGAGTTG**T**TTCCAGTGTTCCCGATGACTTTGATGGACCCTCCAAAACAATTGACTGTGTGACCAATGA	5794
	CACTGGAA**A**CAACTCCA	5795

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGGAGTTG**T**TTCCAGTG	5796
Lys Overproduction DHPS *Nicotiana tabacum* Ala145Val GCA-GTA	GAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCACAAGGGAAGCAATCCATG**T**AACTGAACAGGGATTTGCTGTAGGTATGCATGCAGCTCTTCACATTAATCCCTACTATGG	5797
	CCATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCAAATCCCTGTTCAGTT**A**CATGGATTGCTTCCCTTGTGGAGTTGCTTCCAGTGTTCCCGATGACTTTGATGGACCCTC	5798
	AATCCATG**T**AACTGAAC	5799
	GTTCAGTT**A**CATGGATT	5800
Lys Overproduction DHPS *Nicotiana tabacum* Ala145Thr GCA-ACA	GGAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCACAAGGGAAGCAATCCAT**A**CAACTGAACAGGGATTTGCTGTAGGTATGCATGCAGCTCTTCACATTAATCCCTACTATG	5801
	CATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCAAATCCCTGTTCAGTTG**T**ATGGATTGCTTCCCTTGTGGAGTTGCTTCCAGTGTTCCCGATGACTTTGATGGACCCTCC	5802
	CAATCCAT**A**CAACTGAA	5803
	TTCAGTTG**T**ATGGATTG	5804
Lys Overproduction DHPS *Arabidopsis thaliana* Ser142Asn AGC-AAC	TTATAGGCCATACCGTTAACTGTTTTGGCGGAAGCATCAAAGTCATTGGAAACACTGGAA**A**CAATTCGACTAGAGAAGCAATCCACGCGACTGAACAAGGATTCGCGGTTGGAATGCATGC	5805
	GCATGCATTCCAACCGCGAATCCTTGTTCAGTCGCGTGGATTGCTTCTCTAGTCGAATTG**T**TTCCAGTGTTTCCAATGACTTTGATGCTTCCGCCAAAACAGTTAACGGTATGGCCTATAA	5806
	CACTGGAA**A**CAATTCGA	5807
	TCGAATTG**T**TTCCAGTG	5808
Lys Overproduction DHPS *Arabidopsis thaliana* Ala151Val GCG-GTG	GCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACTAGAGAAGCAATCCACG**T**GACTGAACAAGGATTCGCGGTTGGAATGCATGCTGCTCTTCATATAAACCCTTACTATGG	5809
	CCATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCGAATCCTTGTTCAGTC**A**CGTGGATTGCTTCTCTAGTCGAATTGCTTCCAGTGTTTCCAATGACTTTGATGCTTCCGC	5810
	AATCCACG**T**GACTGAAC	5811
	GTTCAGTC**A**CGTGGATT	5812
Lys Overproduction DHPS *Arabidopsis thaliana* Ala151Thr GCG-ACG	GGCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACTAGAGAAGCAATCCAC**A**CGACTGAACAAGGATTCGCGGTTGGAATGCATGCTGCTCTTCATATAAACCCTTACTATG	5813
	CATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCGAATCCTTGTTCAGTCG**T**GTGGATTGCTTCTCTAGTCGAATTGCTTCCAGTGTTTCCAATGACTTTGATGCTTCCGCC	5814

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAATCCAC**A**CGACTGAA	5815
	TTCAGTCG**T**GTGGATTG	5816
Lys Overproduction DHPS *Glycine max* Ser103Asn AGC-AAC	TTATTGCTCATACAGTCAACTGTTTTGGTGGGAAAATTAAGGTTATTGGAAATACTGGAA**A**CAACTCCACCAGGGAAGCAATTCATGCCACTGAGCAGGGTTTTGCTGTTGGAATGCATGC	5817
	GCATGCATTCCAACAGCAAAACCCTGCTCAGTGGCATGAATTGCTTCCCTGGTGGAGTTG**T**TTCCAGTATTTCCAATAACCTTAATTTTCCCACCAAAACAGTTGACTGTATGAGCAATAA	5818
	TACTGGAA**A**CAACTCCA	5819
	TGGAGTTG**T**TTCCAGTA	5820
Lys Overproduction DHPS *Glycine max* Ala112Val GCC-GTC	GTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACCAGGGAAGCAATTCATG**T**CACTGAGCAGGGTTTTGCTGTTGGAATGCATGCTGCCCTTCACATAAACCCTTACTATGG	5821
	CCATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCAAAACCCTGCTCAGTG**A**CATGAATTGCTTCCCTGGTGGAGTTGCTTCCAGTATTTCCAATAACCTTAATTTTCCCAC	5822
	AATTCATG**T**CACTGAGC	5823
	GCTCAGTG**A**CATGAATT	5824
Lys Overproduction DHPS *Glycine max* Ala112Thr GCC-ACC	GGTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACCAGGGAAGCAATTCAT**A**CCACTGAGCAGGGTTTTGCTGTTGGAATGCATGCTGCCCTTCACATAAACCCTTACTATG	5825
	CATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCAAAACCCTGCTCAGTGG**T**ATGAATTGCTTCCCTGGTGGAGTTGCTTCCAGTATTTCCAATAACCTTAATTTTCCCACC	5826
	CAATTCAT**A**CCACTGAG	5827
	CTCAGTGG**T**ATGAATTG	5828
Trp Overproduction AS *Arabidopsis thaliana* Asp341Asn GAC-AAC	CTTGCAGGAGACATATTTCAGATCGTGCTGAGTCAACGTTTTGAGCGGCGAACATTTGCA**A**ACCCCTTTGAAGTTTATAGAGCACTAAGAGTTGTGAATCCAAGTCCGTATATGGGTTATT	5829
	AATAACCCATATACGGACTTGGATTCACAACTCTTAGTGCTCTATAAACTTCAAAGGGGT**T**TGCAAATGTTCGCCGCTCAAAACGTTGACTCAGCACGATCTGAAATATGTCTCCTGCAAG	5830
	CATTTGCA**A**ACCCCTTT	5831
	AAAGGGGT**T**TGCAAATG	5832
Trp Overproduction AS *Nicotiana tabacum* Asp326Asn GAC-AAC	GCTGCAGGAGACATATTTCAAATCGTTTTAAGTCAACGCTTTGAGAGAAGAACATTTGCT**A**ACCCATTTGAAGTGTACAGAGCATTAAGAATTGTGAATCCAAGCCCATATATGACTTACA	5833

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTAAGTCATATATGGGCTTGGATTCACAATTCTTAATGCTCTGTA CACTTCAAATGGGT**T**AGCAAATGTTCTTCTCTCAAAGCGTTGACTT AAAACGATTTGAAATATGTCTCCTGCAGC	5834
	CATTTGCT**A**ACCCATTT	5835
	AAATGGGT**T**AGCAAATG	5836
Trp Overproduction AS *Oryza sativa* Asp323Asn GAC-AAC	CTAGCTGGTGACATTTTTCAAGTAGTCTTAAGCCAGCGTTTTGAGA GGCGTACATTTGCT**A**ACCCCTTTGAGGTGTACCGTGCATTGCGTA TTGTCAATCCTAGTCCTTATATGGCCTATC	5837
	GATAGGCCATATAAGGACTAGGATTGACAATACGCAATGCACGGT ACACCTCAAAGGGGT**T**AGCAAATGTACGCCTCTCAAAACGCTGGC TTAAGACTACTTGAAAAATGTCACCAGCTAG	5838
	CATTTGCT**A**ACCCCTTT	5839
	AAAGGGGT**T**AGCAAATG	5840
Trp Overproduction AS *Ruta graveolens* Asp354Asn GAC-AAC	CTTGCTGGTGACATATTCCAGATCGTACTAAGTCAGCGTTTTGAAA GGCGAACGTTCGCA**A**ACCCATTTGAAATCTATAGATCACTGAGGA TTGTTAATCCAAGCCCATATATGACTTATT	5841
	AATAAGTCATATATGGGCTTGGATTAACAATCCTCAGTGATCTATA GATTTCAAATGGGT**T**TGCGAACGTTCGCCTTTCAAAACGCTGACTT AGTACGATCTGGAATATGTCACCAGCAAG	5842
	CGTTCGCA**A**ACCCATTT	5843
	AAATGGGT**T**TGCGAACG	5844
Trp Overproduction AS *Catharanthus roseus* Asp354Asn GAT-AAT	CTGGCTGGGGACATATTCCAGCTTGTCCTAAGTCAGCGTTTTGAA CGGCGAACATTTGCA**A**ATCCATTTGAAGTCTACCGAGCATTGAGA ATTGTCAACCCAAGTCCATATATGACTTATT	5845
	AATAAGTCATATATGGACTTGGGTTGACAATTCTCAATGCTCGGTA GACTTCAAATGGAT**T**TGCAAATGTTCGCCGTTCAAAACGCTGACTT AGGACAAGCTGGAATATGTCCCCAGCCAG	5846
	CATTTGCA**A**ATCCATTT	5847
	AAATGGAT**T**TGCAAATG	5848

Example 10

Production of modified starch in plants

A principal aim of biotechnology is the improvement of crop plants for food value, agriculture, and to produce a range of plant-derived raw materials. Along with oils, fats and proteins, polysaccharides constitute the main raw materials derived from plants, and apart from cellulose, the storage polymer starch is the most important polysaccharide raw material. Starch is derived from a range of plants, but maize is the most important cultivated plant for the production of starch.

The polysaccharide starch is a polymer made up of glucose molecules. However, starch is not a homogeneous raw material and is, in fact, a highly complex mixture of various types of molecules which differ from each other, for example, in their degree of polymerization and in the degree of branching of the glucose chains. For example, amylose-starch is a basically non-branched polymer made up of α-1,4-glycosidically branched glucose molecules, and amylopectin-starch is a complex mixture of variously branched glucose chains. The branching results from additional α-1,6-glycosidic linkages. In plants from which starch is typically isolated, for example maize or potato, the starch is approximately 25% amylose-starch and 75% amylopectin-starch.

In maize, various mutants in starch metabolism are known, for example *waxy*, *sugary*, *shrunken* and *opaque-2*. In addition to producing a modified starch, these mutations greatly improve grain quality in maize, and thus expand the use of maize not only as the food but also for the important industrial materials in food chemistry. It would therefore be advantageous to be able readily to obtain mutants in these genes in particular maize genotypes as well as other plants. Such plants can be obtained, for example, using traditional breeding methods and through specific genetic modification by means of recombinant DNA techniques.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 20
Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Arabidopsis thaliana* Ala99Lys GCA-AAA	GAACTTGAGACTGAGAAAAGGGATCCAAGGACAGTTGCTTCCATTATTCTTGGAGGTGGA**AA**AGGAACTCGACTCTTTCCTCTCACAAAACGCCGCGCCAAGCCTGCCGTTCCTATCGGGG	5849
	CCCCGATAGGAACGGCAGGCTTGGCGCGGCGTTTTGTGAGAGGAAAGAGTCGAGTTCCT**TT**TCCACCTCCAAGAATAATGGAAGCAACTGTCCTTGGATCCCTTTTCTCAGTCTCAAGTTC	5850
	GAGGTGGA**AA**AGGAACT	5851
	AGTTCCT**TT**TCCACCTC	5852
Increased Starch ADPGPP *Arabidopsis thaliana* Pro127Leu CCA-CTA	CAAAACGCCGCGCCAAGCCTGCCGTTCCTATCGGGGGAGCCTATAGGTTGATAGATGTAC**T**AATGAGCAATTGTATTAACAGCGGAATCAACAAAGTCTACATACTCACACAATATAACTC	5853
	GAGTTATATTGTGTGAGTATGTAGACTTTGTTGATTCCGCTGTTAATACAATTGCTCATT**A**GTACATCTATCAACCTATAGGCTCCCCCGATAGGAACGGCAGGCTTGGCGCGGCGTTTTG	5854
	AGATGTAC**T**AATGAGCA	5855
	TGCTCATT**A**GTACATCT	5856
Increased Starch ADPGPP *Arabidopsis thaliana* Gly162Asn GGA-AAT	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGCTTACAACTCCAAT**AAT**CTTGGCTTTGGAGATGGCTATGTTGAGGTTCTTGCGGCCACTCAAACGCCAGGAGAATC	5857
	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCATCTCCAAAGCCAAG**ATT**ATTGGAGTTGTAAGCACGGGCTAAATGCCTGTTCAATGATGCTGAGTTATATTGTGTGA	5858
	CTCCAAT**AAT**CTTGGCT	5859
	AGCCAAG**ATT**ATTGGAG	5860
Increased Starch ADPGPP *Arabidopsis thaliana* Gly162Asn GGA-AAC	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGCTTACAACTCCAAT**AAC**CTTGGCTTTGGAGATGGCTATGTTGAGGTTCTTGCGGCCACTCAAACGCCAGGAGAATC	5861
	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCATCTCCAAAGCCAAG**GTT**ATTGGAGTTGTAAGCACGGGCTAAATGCCTGTTCAATGATGCTGAGTTATATTGTGTGA	5862
	CTCCAAT**AAC**CTTGGCT	5863
	AGCCAAG**GTT**ATTGGAG	5864

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Arabidopsis thaliana* Asn100Lys AAT-AAA	GTTTGAGAGAAGAAAGGTAGACCCGCAAAATGTGGCTGCAATCATTCTAGGAGGAGGCAAAGGAGCTAAACTCTTCCCTCTTACAATGAGAGCCGCAACACCAGCTGTAAATATTCATCTT	5865
	AAGATGAATATTTACAGCTGGTGTTGCGGCTCTCATTGTAAGAGGGAAGAGTTTAGCTCCTTTGCCTCCTCCTAGAATGATTGCAGCCACATTTTGCGGGTCTACCTTTCTTCTCTCAAAC	5866
	GGAGGCAAAGGAGCTAA	5867
	TTAGCTCCTTTGCCTCC	5868
Increased Starch ADPGPP *Arabidopsis thaliana* Pro128Leu CCG-CTG	CTTGTGTCTTCAAATTATGTTAGGTTCCTGTTGGTGGATGCTACAGGCTGATCGATATCCTGATGAGTAACTGTATTAACAGCTGCATCAACAAGATATTTGTGCTGACACAGTTCAACTC	5869
	GAGTTGAACTGTGTCAGCACAAATATCTTGTTGATGCAGCTGTTAATACAGTTACTCATCAGGATATCGATCAGCCTGTAGCATCCACCAACAGGAACCTAACATAATTTGAAGACACAAG	5870
	CGATATCCTGATGAGTA	5871
	TACTCATCAGGATATCG	5872
Increased Starch ADPGPP *Arabidopsis thaliana* Gly163Asn GGC-AAT	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAACTTATTTTGGGAAT**AAT**ATAAACTTTGGAGGTGGTTTCGTAGAGGTACAAACACTATGACAATAATAACTCTCAGC	5873
	GCTGAGAGTTATTATTGTCATAGTGTTTGTACCTCTACGAAACCACCTCCAAAGTTTAT**ATT**ATTCCCAAAATAAGTTCGTGCTAAATGTCGATTAAGGGAAGCTGAGTTGAACTGTGTCA	5874
	TGGGAAT**AAT**ATAAACT	5875
	AGTTTAT**ATT**ATTCCCA	5876
Increased Starch ADPGPP *Arabidopsis thaliana* Gly163Asn GGC-AAC	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAACTTATTTTGGGAAT**AAC**ATAAACTTTGGAGGTGGTTTCGTAGAGGTACAAACACTATGACAATAATAACTCTCAGC	5877
	GCTGAGAGTTATTATTGTCATAGTGTTTGTACCTCTACGAAACCACCTCCAAAGTTTAT**GTT**ATTCCCAAAATAAGTTCGTGCTAAATGTCGATTAAGGGAAGCTGAGTTGAACTGTGTCA	5878
	TGGGAAT**AAC**ATAAACT	5879
	AGTTTAT**GTT**ATTCCCA	5880
Increased Starch ADPGPP *Lycopersicon esculentum* Val94Lys GTT-AAA	TTGAGGAACAACCAACGGCAGATCCAAAAGCTGTTGCCTCTGTCATTCTAGGTGGTGGT**AAA**GGAACTCGTCTTTTTCCTCTTACAAGCAGAAGAGCTAAACCAGCTGTTCCTATTGGTGG	5881
	CCACCAATAGGAACAGCTGGTTTAGCTCTTCTGCTTGTAAGAGGAAAAAGACGAGTTCC**TTT**ACCACCACCTAGAATGACAGAGGCAACAGCTTTTGGATCTGCCGTTGGTTGTTCCTCAA	5882
	TGGTGGT**AAA**GGAACTC	5883

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAGTTCC**TTT**ACCACCA	5884
Increased Starch ADPGPP *Lycopersicon esculentum* Pro122Leu CCA-CAA	CAAGCAGAAGAGCTAAACCAGCTGTTCCTATTGGTGGTTGTTACCGGCTAATTGATGTAC**A**AATGAGTAACTGCATTAACAGTGGCATACGGAAAATTTTCATCTTAACACAGTTCAATTC	5885
	GAATTGAACTGTGTTAAGATGAAAATTTTCCGTATGCCACTGTTAATGCAGTTACTCATT**T**GTACATCAATTAGCCGGTAACAACCACCAATAGGAACAGCTGGTTTAGCTCTTCTGCTTG	5886
	TGATGTAC**A**AATGAGTA	5887
	TACTCATT**T**GTACATCA	5888
Increased Starch ADPGPP *Lycopersicon esculentum* Gly158Asn GGA-AAT	CACAGTTCAATTCCTTTTCCCTCAATCGTCACCTTGCCCGCACGTATAATTTTGGAAAT**AAT**GTGGGTTTTGGAGATGGATTTGTGGAGGTTTTAGCTGCAACCCAGACTCCAGGGGATGC	5889
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCATCTCCAAAACCCAC**ATT**ATTTCCAAAATTATACGTGCGGGCAAGGTGACGATTGAGGGAAAAGGAATTGAACTGTG	5890
	TGGAAAT**AAT**GTGGGTT	5891
	AACCCAC**ATT**ATTTCCA	5892
Increased Starch ADPGPP *Lycopersicon esculentum* Gly158Asn GGA-AAC	CACAGTTCAATTCCTTTTCCCTCAATCGTCACCTTGCCCGCACGTATAATTTTGGAAAT**AAC**GTGGGTTTTGGAGATGGATTTGTGGAGGTTTTAGCTGCAACCCAGACTCCAGGGGATGC	5893
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCATCTCCAAAACCCAC**GTT**ATTTCCAAAATTATACGTGCGGGCAAGGTGACGATTGAGGGAAAAGGAATTGAACTGTG	5894
	TGGAAAT**AAC**GTGGGTT	5895
	AACCCAC**GTT**ATTTCCA	5896
Increased Starch ADPGPP *Cicer arietinum* Ala101Lys GCT-AAA	ACGTAGATTTGGAAAAAAGAGACCCAAGTACAGTTGTAGCAATTATACTAGGTGGAGGT**AAA**GGAACTCGTCTCTTCCCTCTCACCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGG	5897
	CCTCCAATTGGAACAGCAGGCTTGGCTCGTCGCTTGGTGAGAGGGAAGAGACGAGTTCC**TTT**ACCTCCACCTAGTATAATTGCTACAACTGTACTTGGGTCTCTTTTTTCCAAATCTACGT	5898
	TGGAGGT**AAA**GGAACTC	5899
	GAGTTCC**TTT**ACCTCCA	5900

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Cicer arietinum* Pro129Leu CCA-CTA	CCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGGTGCTTATAGGCTGATAGATGTAC**T**AATGAGTAACTGCATCAATAGTGGGATCAACAAAGTATACATTCTCACTCAATTTAATTC	5901
	GAATTAAATTGAGTGAGAATGTATACTTTGTTGATCCCACTATTGATGCAGTTACTCATT**A**GTACATCTATCAGCCTATAAGCACCTCCAATTGGAACAGCAGGCTTGGCTCGTCGCTTGG	5902
	AGATGTAC**T**AATGAGTA	5903
	TACTCATT**A**GTACATCT	5904
Increased Starch ADPGPP *Cicer arietinum* Gly165Asn GGA-AAT	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTATAACTCTGGTACT**AAT**GTCACTTTTGGAGATGGCTATGTTGAGGTTCTTGCAGCAACTCAAACTCCAGGGGAGCA	5905
	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCATCTCCAAAAGTGAC**ATT**AGTACCAGAGTTATAAGCACGTGCAATATGCCTGTTGAGTGAGGCTGAATTAAATTGAG	5906
	TGGTACT**AAT**GTCACTT	5907
	AAGTGAC**ATT**AGTACCA	5908
Increased Starch ADPGPP *Cicer arietinum* Gly165Asn GGA-AAC	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTATAACTCTGGTACT**AAC**GTCACTTTTGGAGATGGCTATGTTGAGGTTCTTGCAGCAACTCAAACTCCAGGGGAGCA	5909
	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCATCTCCAAAAGTGAC**GTT**AGTACCAGAGTTATAAGCACGTGCAATATGCCTGTTGAGTGAGGCTGAATTAAATTGAG	5910
	TGGTACT**AAC**GTCACTT	5911
	AAGTGAC**GTT**AGTACCA	5912
Increased Starch ADPGPP *Ipomoea batatas* Ala94Lys GCA-AAA	ATATTGGAGAGGCGTCGGGCAAACCCTAAGAATGTGGCTGCAATCATACTGCCAGGCGGT**AA**AGGGACACACCTATTCCCTCTCACCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAG	5913
	CTCCAAGTGGAACAGCAGGGGTTGCAGCTCGATTGGTGAGAGGGAATAGGTGTGTCCCT**TT**ACCGCCTGGCAGTATGATTGCAGCCACATTCTTAGGGTTTGCCCGACGCCTCTCCAATAT	5914
	CAGGCGGT**AA**AGGGACA	5915
	TGTCCCT**TT**ACCGCCTG	5916
Increased Starch ADPGPP *Ipomoea batatas* Pro122Leu CCA-CTA	CCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAGGATGCTATAGGTTGATCGACATTC**T**AATGAGCAACTGCATCAACAGCGGGGTTAACAAGATCTTTGTGCTGACCCAGTTCAATTC	5917
	GAATTGAACTGGGTCAGCACAAAGATCTTGTTAACCCCGCTGTTGATGCAGTTGCTCATT**A**GAATGTCGATCAACCTATAGCATCCTCCAAGTGGAACAGCAGGGGTTGCAGCTCGATTGG	5918
	CGACATTC**T**AATGAGCA	5919

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCTCATTAGAATGTCG	5920
Increased Starch ADPGPP *Ipomoea batatas* Gly157Asn GGT-AAT	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC CGTCTTTGGCAAT**AAT**GTGAGCTTCGGAGATGGATTTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	5921
	GTTTCCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCAC**ATT**ATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACTGGGTCA	5922
	TGGCAAT**AAT**GTGAGCT	5923
	AGCTCAC**ATT**ATTGCCA	5924
Increased Starch ADPGPP *Ipomoea batatas* Gly157Asn GGT-AAC	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC CGTCTTTGGCAAT**AAC**GTGAGCTTCGGAGATGGATTTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	5925
	GTTTCCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCAC**GTT**ATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACTGGGTCA	5926
	TGGCAAT**AAC**GTGAGCT	5927
	AGCTCAC**GTT**ATTGCCA	5928
Increased Starch ADPGPP *Oryza sativa* Thr96Lys ACC-AAA	CATTCCGGAGGAACTTTGCGGATCCAAATGAGGTTGCTGCTGTTA TATTGGGTGGTGGCA**AA**GGGACTCAACTTTTTCCTCTCACAAGCA CAAGGGCCACGCCTGCTGTTCCTATTGGAGG	5929
	CCTCCAATAGGAACAGCAGGCGTGGCCCTTGTGCTTGTGAGAGG AAAAAGTTGAGTCCC**TT**TGCCACCACCCAATATAACAGCAGCAAC CTCATTTGGATCCGCAAAGTTCCTCCGGAATG	5930
	TGGTGGCA**AA**GGGACTC	5931
	GAGTCCC**TT**TGCCACCA	5932
Increased Starch ADPGPP *Oryza sativa* Pro124Leu CCC-CTC	CAAGCACAAGGGCCACGCCTGCTGTTCCTATTGGAGGATGCTATA GGCTTATCGATATCC**T**CATGAGCAACTGTTTCAACAGTGGCATAAA CAAGATATTCATAATGACTCAATTCAACTC	5933
	GAGTTGAATTGAGTCATTATGAATATCTTGTTTATGCCACTGTTGAA ACAGTTGCTCATG**A**GGATATCGATAAGCCTATAGCATCCTCCAATA GGAACAGCAGGCGTGGCCCTTGTGCTTG	5934
	CGATATCC**T**CATGAGCA	5935
	TGCTCATG**A**GGATATCG	5936
Increased Starch ADPGPP *Oryza sativa* Gly159Asn GGA-AAT	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGGTGGT**AAT**ATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC	5937
	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGAT**ATT**ACCACCAAGGTACGTACGATGAATGTGAC GATTAAGAGATGCTGAGTTGAATTGAGTCA	5938

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGGTGGT**AAT**ATCAACT	5939
	AGTTGAT**ATT**ACCACCA	5940
Increased Starch ADPGPP *Oryza sativa* Gly159Asn GGA-AAC	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGGTGGT**AAC**ATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC	5941
	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGAT**GTT**ACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA	5942
	TGGTGGT**AAC**ATCAACT	5943
	AGTTGAT**GTT**ACCACCA	5944
Increased Starch ADPGPP *Triticum aestivum* Thr80Lys ACC-AAA	GTCCTTCAGGAGGATTAAGCGATCCGAACGAGGTTGCGGCCGTC ATACTCGGCGGCGGCA**AA**GGGACTCAGCTCTTCCCACTCACGAG CACAAGGGCCACACCTGCTGTTCCTATTGGAGG	5945
	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTCGTGAGTGG GAAGAGCTGAGTCCC**TT**TGCCGCCGCCGAGTATGACGGCCGCAA CCTCGTTCGGATCGCTTAATCCTCCTGAAGGAC	5946
	CGGCGGCA**AA**GGGACTC	5947
	GAGTCCC**TT**TGCCGCCG	5948
Increased Starch ADPGPP *Triticum aestivum* Pro108Leu CCC-CTC	CGAGCACAAGGGCCACACCTGCTGTTCCTATTGGAGGATGTTACA GGCTCATCGACATTC**T**CATGAGCAACTGCTTCAACAGTGGCATCA ACAAGATATTCGTCATGACCCAGTTCAACTC	5949
	GAGTTGAACTGGGTCATGACGAATATCTTGTTGATGCCACTGTTG AAGCAGTTGCTCATG**A**GAATGTCGATGAGCCTGTAACATCCTCCA ATAGGAACAGCAGGTGTGGCCCTTGTGCTCG	5950
	CGACATTC**T**CATGAGCA	5951
	TGCTCATG**A**GAATGTCG	5952
Increased Starch ADPGPP *Triticum aestivum* Gly143Asn GGA-AAT	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG**AAT**ATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5953
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGAT**ATT**CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	5954
	CGGCGGG**AAT**ATCAATT	5955
	AATTGAT**ATT**CCCGCCG	5956
Increased Starch ADPGPP *Triticum aestivum* Gly143Asn GGA-AAC	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG**AAC**ATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5957

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGAT**GTT**CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	5958
	CGGCGGG**AAC**ATCAATT	5959
	AATTGAT**GTT**CCCGCCG	5960
Increased Starch ADPGPP *Oryza sativa* Thr95Lys ACT-AAA	CCTCCCGAAAGAATTATGCTGATGCAAGCCACGTTTCTGCTGTCA TTTTGGGTGGAGGCA**AA**GGAGTTCAACTCTTTCCTCTGACAAGCA CAAGGGCTACCCCCGCTGTTCCTGTTGGAGG	5961
	CCTCCAACAGGAACAGCGGGGGTAGCCCTTGTGCTTGTCAGAGG AAAGAGTTGAACTCC**TT**TGCCTCCACCCAAAATGACAGCAGAAAC GTGGCTTGCATCAGCATAATTCTTTCGGGAGG	5962
	TGGAGGCA**AA**GGAGTTC	5963
	GAACTCC**TT**TGCCTCCA	5964
Increased Starch ADPGPP *Oryza sativa* Pro123Leu CCT-CTT	CAAGCACAAGGGCTACCCCCGCTGTTCCTGTTGGAGGATGTTACA GGCTTATTGACATCC**T**TATGAGCAATTGCTTCAATAGCGGAATAAA TAAAATATTTGTGATGACTCAGTTCAATTC	5965
	GAATTGAACTGAGTCATCACAAATATTTTATTTATTCCGCTATTGAA GCAATTGCTCATA**A**GGATGTCAATAAGCCTGTAACATCCTCCAACA GGAACAGCGGGGGTAGCCCTTGTGCTTG	5966
	TGACATCC**T**TATGAGCA	5967
	TGCTCATA**A**GGATGTCA	5968
Increased Starch ADPGPP *Oryza sativa* Gly158Asn GGG-AAT	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATAC ATACCTTGGTGGG**AAT**ATCAACTTTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCTGACGAACC	5969
	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGAT**ATT**CCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGAACTGAGTCA	5970
	TGGTGGG**AAT**ATCAACT	5971
	AGTTGAT**ATT**CCCACCA	5972
Increased Starch ADPGPP *Oryza sativa* Gly158Asn GGG-AAC	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATAC ATACCTTGGTGGG**AAC**ATCAACTTTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCTGACGAACC	5973
	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGAT**GTT**CCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGAACTGAGTCA	5974
	TGGTGGG**AAC**ATCAACT	5975
	AGTTGAT**GTT**CCCACCA	5976

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Triticum aestivum* Thr99Lys ACC-AAA	CCTTCCGCAGGAATTACGCCGATCCGAACGAGGTCGCGGCCGTC ATACTCGGCGGTGGCA**AA**GGGACTCAGCTCTTCCCTCTCACAAG CACAAGGGCCACACCTGCTGTTCCTATTGGAGG	5977
	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTTGTGAGAGG GAAGAGCTGAGTCCC**TT**TGCCACCGCCGAGTATGACGGCCGCGA CCTCGTTCGGATCGGCGTAATTCCTGCGGAAGG	5978
	CGGTGGCA**AA**GGGACTC	5979
	GAGTCCC**TT**TGCCACCG	5980
Increased Starch ADPGPP *Triticum aestivum* Pro127Leu CCC-CTC	CAAGCACAAGGGCCACACCTGCTGTTCCTATTGGAGGATGTTACA GGCTCATCGATATTC**T**CATGAGCAACTGCTTCAATAGTGGCATCAA CAAGATATTCGTCATGACGCAGTTCAACTC	5981
	GAGTTGAACTGCGTCATGACGAATATCTTGTTGATGCCACTATTGA AGCAGTTGCTCATG**A**GAATATCGATGAGCCTGTAACATCCTCCAA TAGGAACAGCAGGTGTGGCCCTTGTGCTTG	5982
	CGATATTC**T**CATGAGCA	5983
	TGCTCATG**A**GAATATCG	5984
Increased Starch ADPGPP *Triticum aestivum* Gly162Asn GGA-AAT	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG**AAT**ATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5985
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGAT**ATT**CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	5986
	CGGCGGG**AAT**ATCAATT	5987
	AATTGAT**ATT**CCCGCCG	5988
Increased Starch ADPGPP *Triticum aestivum* Gly162Asn GGA-AAC	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG**AAC**ATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5989
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGAT**GTT**CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	5990
	CGGCGGG**AAC**ATCAATT	5991
	AATTGAT**GTT**CCCGCCG	5992
Increased Starch ADPGPP *Zea mays* Thr96Lys ACC-AAA	CTTTTCGGAGGAATTATGCTGATCCTAATGAAGTCGCTGCCGTCA TTTTGGGTGGTGGTA**AA**GGGACTCAGCTTTTCCCTCTCACAAGCA CAAGGGCCACCCCTGCTGTTCCTATTGGAGG	5993
	CCTCCAATAGGAACAGCAGGGGTGGCCCTTGTGCTTGTGAGAGG GAAAAGCTGAGTCCC**TT**TACCACCACCCAAAATGACGGCAGCGAC TTCATTAGGATCAGCATAATTCCTCCGAAAAG	5994
	TGGTGGTA**AA**GGGACTC	5995

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAGTCCCTTTACCACCA	5996
Increased Starch ADPGPP *Zea mays* Pro124Leu CCC-CTC	CAAGCACAAGGGCCACCCCTGCTGTTCCTATTGGAGGATGTTACA GGCTTATTGATATCCTCATGAGCAACTGTTTCAACAGTGGCATAAA CAAGATATTTGTTATGACTCAGTTCAACTC	5997
	GAGTTGAACTGAGTCATAACAAATATCTTGTTTATGCCACTGTTGA AACAGTTGCTCATGAGGATATCAATAAGCCTGTAACATCCTCCAAT AGGAACAGCAGGGGTGGCCCTTGTGCTTG	5998
	TGATATCCTCATGAGCA	5999
	TGCTCATGAGGATATCA	6000
Increased Starch ADPGPP *Zea mays* Gly159Asn GGG-AAT	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC CTATCTTGGTGGG**AAT**ATCAACTTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC	6001
	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGAT**ATT**CCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	6002
	TGGTGGG**AAT**ATCAACT	6003
	AGTTGAT**ATT**CCCACCA	6004
Increased Starch ADPGPP *Zea mays* Gly159Asn GGG-AAC	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC CTATCTTGGTGGG**AAC**ATCAACTTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC	6005
	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGAT**GTT**CCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	6006
	TGGTGGG**AAC**ATCAACT	6007
	AGTTGAT**GTT**CCCACCA	6008
Increased Starch ADPGPP *Solanum tuberosum* Ala58Lys GCG-AAG	CTTGAGAGGCAAAAGAAGGGCGATGCAAGGACAGTAGTAGCAAT CATTCTAGGAGGGGGA**AA**GGGAACTCGTCTTTTCCCCCTCACCAA ACGTCGTGCTAAGCCTGCCGTTCCAATGGGAG	6009
	CTCCCATTGGAACGGCAGGCTTAGCACGACGTTTGGTGAGGGGG AAAAGACGAGTTCCCTTTCCCCCTCCTAGAATGATTGCTACTACTG TCCTTGCATCGCCCTTCTTTTGCCTCTCAAG	6010
	GAGGGGGA**AA**GGGAACT	6011
	AGTTCCCTTTCCCCCTC	6012
Increased Starch ADPGPP *Solanum tuberosum* Pro86Leu CCA-CTA	CCAAACGTCGTGCTAAGCCTGCCGTTCCAATGGGAGGAGCATATA GGCTAATTGATGTACTAATGAGCAACTGTATTAACAGTGGCATCAA CAAAGTATACATTCTCACTCAATTCAACTC	6013
	GAGTTGAATTGAGTGAGAATGTATACTTTGTTGATGCCACTGTTAA TACAGTTGCTCATTAGTACATCAATTAGCCTATATGCTCCTCCCAT TGGAACGGCAGGCTTAGCACGACGTTTGG	6014

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATGTAC**T**AATGAGCA	6015
	TGCTCATT**A**GTACATCA	6016
Increased Starch ADPGPP *Solanum tuberosum* Gly122Asn GGG-AAT	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAAT**AAT**GTCACATTCGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6017
	AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCA CTCTCGAATGTGAC**ATT**ATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTTAAGTGAGGCTGAGTTGAATTGAG	6018
	TGGCAAT**AAT**GTCACAT	6019
	ATGTGAC**ATT**ATTGCCA	6020
Increased Starch ADPGPP *Solanum tuberosum* Gly122Asn GGG-AAC	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAAT**AAC**GTCACATTCGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6021
	AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCA CTCTCGAATGTGAC**GTT**ATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTTAAGTGAGGCTGAGTTGAATTGAG	6022
	TGGCAAT**AAC**GTCACAT	6023
	ATGTGAC**GTT**ATTGCCA	6024
Increased Starch ADPGPP *Beta vulgaris* Ala98Lys GCT-AAA	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGT**AAA**GGGACTCGCCTCTTTCCTCTTACTAGCA GGAGAGCTAAGCCAGCAGTGCCAATTGGAGG	6025
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCC**TTT**ACCACCACCCAGCACAATTGCAGCCACA TTTTTTGGGTCAGCTTTTGGAGATTCAAATA	6026
	TGGTGGT**AAA**GGGACTC	6027
	GAGTCCC**TTT**ACCACCA	6028
Increased Starch ADPGPP *Beta vulgaris* Ala98Lys GCT-AAC	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGT**AAC**GGGACTCGCCTCTTTCCTCTTACTAGCA GGAGAGCTAAGCCAGCAGTGCCAATTGGAGG	6029
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCC**GTT**ACCACCACCCAGCACAATTGCAGCCAC ATTTTTTGGGTCAGCTTTTGGAGATTCAAATA	6030
	TGGTGGT**AAC**GGGACTC	6031
	GAGTCCC**GTT**ACCACCA	6032
Increased Starch ADPGPP *Beta vulgaris* Pro126Leu CCT-CTT	CTAGCAGGAGAGCTAAGCCAGCAGTGCCAATTGGAGGGTGTTAC AGGCTGATTGATGTGC**T**TATGAGCAACTGCATCAACAGTGGCATT AGAAAGATTTTCATTCTTACCCAGTTCAATTC	6033

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAATTGAACTGGGTAAGAATGAAAATCTTTCTAATGCCACTGTTGATGCAGTTGCTCATAAGCACATCAATCAGCCTGTAACACCCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAG	6034
	TGATGTGCTTATGAGCA	6035
	TGCTCATAAGCACATCA	6036
Increased Starch ADPGPP *Beta vulgaris* Gly162Asn GGT-AAT	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTATAATTTTGGAGAT**AAT**GTGAATTTTGGGGATGGCTTTGTGGAGGTTTTTGCTGCTACACAAACACCTGGAGAATC	6037
	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCATCCCCAAAATTCAC**ATT**ATCTCCAAAATTATAGGTTCGAGCAAGATGACGATTAAGCGAAAACGAATTGAACTGGG	6038
	TGGAGAT**AAT**GTGAATT	6039
	AATTCAC**ATT**ATCTCCA	6040
Increased Starch ADPGPP *Beta vulgaris* Gly162Asn GGT-AAC	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTATAATTTTGGAGAT**AAC**GTGAATTTTGGGGATGGCTTTGTGGAGGTTTTTGCTGCTACACAAACACCTGGAGAATC	6041
	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCATCCCCAAAATTCAC**GTT**ATCTCCAAAATTATAGGTTCGAGCAAGATGACGATTAAGCGAAAACGAATTGAACTGGG	6042
	TGGAGAT**AAC**GTGAATT	6043
	AATTCAC**GTT**ATCTCCA	6044

Table 21
Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Arabidopsis thaliana* Ser12Term TCA-TGA	GAATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTTCTAACTTTGTGT**G**AAGAACTTCACTTTTCAACAATCATGGTGCTTCTTCATGCTCTGATGTCGCTCAGATTAC	6045
	GTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTGAAAAGTGAAGTTCTT**C**ACACAAAGTTAGAAGAAGCAGTCACAGTTGCCATTATGAACTACCCGTTTACCTGGATTC	6046
	CTTTGTGT**G**AAGAACTT	6047
	AAGTTCTT**C**ACACAAAG	6048
Waxy starch GBSS *Arabidopsis thaliana* Arg13Term AGA-TGA	ATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTTCTAACTTTGTGTCA**T**GAACTTCACTTTTCAACAATCATGGTGCTTCTTCATGCTCTGATGTCGCTCAGATTACCT	6049
	AGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTGAAAAGTGAAGTTC**A**TGACACAAAGTTAGAAGAAGCAGTCACAGTTGCCATTATGAACTACCCGTTTACCTGGAT	6050
	TTGTGTCA**T**GAACTTCA	6051
	TGAAGTTC**A**TGACACAA	6052
Waxy starch GBSS *Arabidopsis thaliana* Ser15Term TCA-TGA	TAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTTCTAACTTTGTGTCAAGAACTT**G**ACTTTTCAACAATCATGGTGCTTCTTCATGCTCTGATGTCGCTCAGATTACCTTAAAAGG	6053
	CCTTTTAAGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTGAAAAGT**C**AAGTTCTTGACACAAAGTTAGAAGAAGCAGTCACAGTTGCCATTATGAACTACCCGTTTA	6054
	AAGAACTT**G**ACTTTTCA	6055
	TGAAAAGT**C**AAGTTCTT	6056
Waxy starch GBSS *Arabidopsis thaliana* Ser24Term TCA-TGA	TGACTGCTTCTTCTAACTTTGTGTCAAGAACTTCACTTTTCAACAATCATGGTGCTTCTT**G**ATGCTCTGATGTCGCTCAGATTACCTTAAAAGGCCAATCCTTGACTCATTGTGGGTTAAG	6057
	CTTAACCCACAATGAGTCAAGGATTGGCCTTTTAAGGTAATCTGAGCGACATCAGAGCAT**C**AAGAAGCACCATGATTGTTGAAAAGTGAAGTTCTTGACACAAAGTTAGAAGAAGCAGTCA	6058
	TGCTTCTT**G**ATGCTCTG	6059
	CAGAGCAT**C**AAGAAGCA	6060

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Arabidopsis thaliana* Cys25Term TGC-TGA	TGCTTCTTCTAACTTTGTGTCAAGAACTTCACTTTTCAACAATCATG GTGCTTCTTCATG**A**TCTGATGTCGCTCAGATTACCTTAAAAGGCCA ATCCTTGACTCATTGTGGGTTAAGGTCA	6061
	TGACCTTAACCCACAATGAGTCAAGGATTGGCCTTTTAAGGTAATC TGAGCGACATCAGA**T**CATGAAGAAGCACCATGATTGTTGAAAAGTG AAGTTCTTGACACAAAGTTAGAAGAAGCA	6062
	TCTTCATG**A**TCTGATGT	6063
	ACATCAGA**T**CATGAAGA	6064
Waxy starch GBSS *Antirrhinum majus* Lys24Term AAA-TAA	GTAACAGCTTCACAGTTGGTGTCACATGTCCATGGTGGAGCAACG TCTTCACCGGATACT**T**AAACAAACTTGGCCCAGGTTGGCCTCAGG AACCAGCAATTCACTCACAATGGGTTGAGAT	6065
	ATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGAGGCCAACCT GGGCCAAGTTTGTTT**A**AGTATCCGGTGAAGACGTTGCTCCACCAT GGACATGTGACACCAACTGTGAAGCTGTTAC	6066
	CGGATACT**T**AAACAAAC	6067
	GTTTGTTT**A**AGTATCCG	6068
Waxy starch GBSS *Antirrhinum majus* Leu27Term TTG-TAG	CACAGTTGGTGTCACATGTCCATGGTGGAGCAACGTCTTCACCGG ATACTAAAACAAACT**A**GGCCCAGGTTGGCCTCAGGAACCAGCAAT TCACTCACAATGGGTTGAGATCAATAAACAT	6069
	ATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGA GGCCAACCTGGGCC**T**AGTTTGTTTTAGTATCCGGTGAAGACGTTG CTCCACCATGGACATGTGACACCAACTGTG	6070
	AACAAACT**A**GGCCCAGG	6071
	CCTGGGCC**T**AGTTTGTT	6072
Waxy starch GBSS *Antirrhinum majus* Gln29Term CAG-TAG	TTGGTGTCACATGTCCATGGTGGAGCAACGTCTTCACCGGATACT AAAACAAACTTGGCC**T**AGGTTGGCCTCAGGAACCAGCAATTCACT CACAATGGGTTGAGATCAATAAACATGGTTG	6073
	CAACCATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGTT CCTGAGGCCAACCT**A**GGCCAAGTTTGTTTTAGTATCCGGTGAAGA CGTTGCTCCACCATGGACATGTGACACCAA	6074
	ACTTGGCC**T**AGGTTGGC	6075
	GCCAACCT**A**GGCCAAGT	6076
Waxy starch GBSS *Antirrhinum majus* Gln35Term CAG-TAG	GGTGGAGCAACGTCTTCACCGGATACTAAAACAAACTTGGCCCAG GTTGGCCTCAGGAAC**T**AGCAATTCACTCACAATGGGTTGAGATCAA TAAACATGGTTGATAAGCTTCAAATGAGGA	6077
	TCCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCATTG TGAGTGAATTGCT**A**GTTCCTGAGGCCAACCTGGGCCAAGTTTGTT TTAGTATCCGGTGAAGACGTTGCTCCACC	6078

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCAGGAAC**T**AGCAATTC	6079
	GAATTGCT**A**GTTCCTGA	6080
Waxy starch GBSS *Antirrhinum majus* Gln36Term CAA-TAA	GGAGCAACGTCTTCACCGGATACTAAAACAAACTTGGCCCAGGTTGGCCTCAGGAACCAG**T**AATTCACTCACAATGGGTTGAGATCAATAAACATGGTTGATAAGCTTCAAATGAGGAACA	6081
	TGTTCCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCATTGTGAGTGAATT**A**CTGGTTCCTGAGGCCAACCTGGGCCAAGTTTGTTTTAGTATCCGGTGAAGACGTTGCTCC	6082
	GGAACCAG**T**AATTCACT	6083
	AGTGAATT**A**CTGGTTCC	6084
Waxy starch GBSS *Ipomoea batatas* Gly20Term GGA-TGA	GTGATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCT**T**GAGAATCAAAAGTGGGGTTGGGTCAATTAGCCCTGAGGAGCCAAGCTGTGACTCACAATG	6085
	CATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACCCCACTTTTGATTCTC**A**AGAAGTGGCACCCCCACAGACATGAGAAACAAAGTGTGAGGCAGTTATAGTCGCCATCAC	6086
	CCACTTCT**T**GAGAATCA	6087
	TGATTCTC**A**AGAAGTGG	6088
Waxy starch GBSS *Ipomoea batatas* Glu21Term GAA-TAA	ATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGA**T**AATCAAAAGTGGGGTTGGGTCAATTAGCCCTGAGGAGCCAAGCTGTGACTCACAATGGGT	6089
	ACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACCCCACTTTTGATT**A**TCCAGAAGTGGCACCCCCACAGACATGAGAAACAAAGTGTGAGGCAGTTATAGTCGCCAT	6090
	CTTCTGGA**T**AATCAAAA	6091
	TTTTGATT**A**TCCAGAAG	6092
Waxy starch GBSS *Ipomoea batatas* Ser22Term TCA-TGA	CGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGAGAAT**G**AAAAGTGGGGTTGGGTCAATTAGCCCTGAGGAGCCAAGCTGTGACTCACAATGGGTTGAG	6093
	CTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACCCCACTTTT**C**ATTCTCCAGAAGTGGCACCCCCACAGACATGAGAAACAAAGTGTGAGGCAGTTATAGTCG	6094
	TGGAGAAT**G**AAAAGTGG	6095
	CCACTTTT**C**ATTCTCCA	6096

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Ipomoea batatas* Lys23Term AAA-TAA	ACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGAGAATCA**T**AAGTGGGGTTGGGTCAATTAGCCCTGAGGAGCCAAGCTGTGACTCACAATGGGTTGAGAC	6097
	GTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACCCCACTT**A**TGATTCTCCAGAAGTGGCACCCCCACAGACATGAGAAACAAAGTGTGAGGCAGTTATAGT	6098
	GAGAATCA**T**AAGTGGGG	6099
	CCCCACTT**A**TGATTCTC	6100
Waxy starch GBSS *Ipomoea batatas* Leu26Term TTG-TAG	CCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGAGAATCAAAAGTGGGGT**A**GGGTCAATTAGCCCTGAGGAGCCAAGCTGTGACTCACAATGGGTTGAGACCTGTGAACAA	6101
	TTGTTCACAGGTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCC**T**ACCCCACTTTTGATTCTCCAGAAGTGGCACCCCCACAGACATGAGAAACAAAGTGTGAGG	6102
	AGTGGGGT**A**GGGTCAAT	6103
	ATTGACCC**T**ACCCCACT	6104
Waxy starch GBSS *Astragalus membranaeus* Tyr8Term TAT-TAG	CATCGGCGATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGGGGTCTTA**G**GTGGTGTCGAGAAGCGCGTGCTTCAATTCCCAGGGAAGAACAGAAGCCAAAGTGAATTCA	6105
	TGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATTGAAGCACGCGCTTCTCGACACCAC**C**TAAGACCCCGTCACCGTTGCCATTCTGTGAGAGAGCAGTAAGGAGCAACAATCGCCGATG	6106
	GGGTCTTA**G**GTGGTGTC	6107
	GACACCAC**C**TAAGACCC	6108
Waxy starch GBSS *Astragalus membranaeus* Ser11Term TCG-TAG	ATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGGGGTCTTATGTGGTGT**A**GAGAAGCGCGTGCTTCAATTCCCAGGGAAGAACAGAAGCCAAAGTGAATTCACCTCAGAA	6109
	TTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATTGAAGCACGCGCTTCTC**T**ACACCACATAAGACCCCGTCACCGTTGCCATTCTGTGAGAGAGCAGTAAGGAGCAACAAT	6110
	TGTGGTGT**A**GAGAAGCG	6111
	CGCTTCTC**T**ACACCACA	6112

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Astragalus membranaeus* Arg12Term AGA-TGA	TGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGGGG TCTTATGTGGTGTCG**T**GAAGCGCGTGCTTCAATTCCCAGGGAAGA ACAGAAGCCAAAGTGAATTCACCTCAGAAGA	6113
	TCTTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATT GAAGCACGCGCTTC**A**CGACACCACATAAGACCCCGTCACCGTTGC CATTCTGTGAGAGAGCAGTAAGGAGCAACA	6114
	TGGTGTCG**T**GAAGCGCG	6115
	CGCGCTTC**A**CGACACCA	6116
Waxy starch GBSS *Astragalus membranaeus* Cys15Term TGC-TGA	ACTGCTCTCTCACAGAATGGCAACGGTGACGGGGTCTTATGTGGT GTCGAGAAGCGCGTG**A**TTCAATTCCCAGGGAAGAACAGAAGCCAA AGTGAATTCACCTCAGAAGATAAATCTCAAT	6117
	ATTGAGATTTATCTTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTC CCTGGGAATTGAA**T**CACGCGCTTCTCGACACCACATAAGACCCCG TCACCGTTGCCATTCTGTGAGAGAGCAGT	6118
	AGCGCGTG**A**TTCAATTC	6119
	GAATTGAA**T**CACGCGCT	6120
Waxy starch GBSS *Astragalus membranaeus* Gln19Term CAG-TAG	CACAGAATGGCAACGGTGACGGGGTCTTATGTGGTGTCGAGAAGC GCGTGCTTCAATTCC**T**AGGGAAGAACAGAAGCCAAAGTGAATTCA CCTCAGAAGATAAATCTCAATAGCCAAGCAT	6121
	ATGCTTGGCTATTGAGATTTATCTTCTGAGGTGAATTCACTTTGGCT TCTGTTCTTCCCT**A**GGAATTGAAGCACGCGCTTCTCGACACCACAT AAGACCCCGTCACCGTTGCCATTCTGTG	6122
	TCAATTCC**T**AGGGAAGA	6123
	TCTTCCCT**A**GGAATTGA	6124
Waxy starch GBSS *Solanum tuberosum* Ser7Term TCA-TGA	TGTAGCTTGGTAGATTCCCCTTTTTGTAGACCACACATCACATGGC AAGCATCACAGCTT**G**ACACCACTTTGTGTCAAGAAGCCAAACTTCA CTAGACACCAAATCAACCTTGTCACAGAT	6125
	ATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTTGGCTTCTTG ACACAAAGTGGTGT**C**AAGCTGTGATGCTTGCCATGTGATGTGTGG TCTACAAAAAGGGGAATCTACCAAGCTACA	6126
	CACAGCTT**G**ACACCACT	6127
	AGTGGTGT**C**AAGCTGTG	6128
Waxy starch GBSS *Solanum tuberosum* Ser12Term TCA-TGA	TCCCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTC ACACCACTTTGTGT**G**AAGAAGCCAAACTTCACTAGACACCAAATCA ACCTTGTCACAGATAGGACTCAGGAACCA	6129
	TGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGTG AAGTTTGGCTTCTT**C**ACACAAAGTGGTGTGAAGCTGTGATGCTTGC CATGTGATGTGTGGTCTACAAAAAGGGGA	6130

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTTTGTGT**G**AAGAAGCC	6131
	GGCTTCTT**C**ACACAAAG	6132
Waxy starch GBSS *Solanum tuberosum* Arg13Term AGA-TGA	CCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTCA**T**GAAGCCAAACTTCACTAGACACCAAATCAACCTTGTCACAGATAGGACTCAGGAACCATA	6133
	TATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTTGGCTTC**A**TGACACAAAGTGGTGTGAAGCTGTGATGCTTGCCATGTGATGTGTGGTCTACAAAAAGGG	6134
	TTGTGTCA**T**GAAGCCAA	6135
	TTGGCTTC**A**TGACACAA	6136
Waxy starch GBSS *Solanum tuberosum* Gln15Term CAA-TAA	TTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTCAAGAAGC**T**AAACTTCACTAGACACCAAATCAACCTTGTCACAGATAGGACTCAGGAACCATACTCTGA	6137
	TCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTT**A**GCTTCTTGACACAAAGTGGTGTGAAGCTGTGATGCTTGCCATGTGATGTGTGGTCTACAA	6138
	CAAGAAGC**T**AAACTTCA	6139
	TGAAGTTT**A**GCTTCTTG	6140
Waxy starch GBSS *Solanum tuberosum* Ser17Term TCA-TGA	CCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTCAAGAAGCCAAACTT**G**ACTAGACACCAAATCAACCTTGTCACAGATAGGACTCAGGAACCATACTCTGACTCACAA	6141
	TTGTGAGTCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGT**C**AAGTTTGGCTTCTTGACACAAAGTGGTGTGAAGCTGTGATGCTTGCCATGTGATGTGTGG	6142
	CCAAACTT**G**ACTAGACA	6143
	TGTCTAGT**C**AAGTTTGG	6144
Waxy starch GBSS *Pisum sativum* Gly6Term GGA-TGA	GTCGATCACTCTTCTCTCACCGCCGAAACAGATTTTGACACAAAAATGGCAACAATAACG**T**GATCTTCAATGCCGACGAGAACCGCGTGCTTCAATTACCAAGGAAGATCAGCAGAGTCTA	6145
	TAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGGTTCTCGTCGGCATTGAAGATC**A**CGTTATTGTTGCCATTTTTGTGTCAAAATCTGTTTCGGCGGTGAGAGAAGAGTGATCGAC	6146
	CAATAACG**T**GATCTTCA	6147
	TGAAGATC**A**CGTTATTG	6148

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Pisum sativum* Ser8Term TCA-TGA	ACTCTTCTCTCACCGCCGAAACAGATTTTGACACAAAAATGGCAACAATAACGGGATCTT**G**AATGCCGACGAGAACCGCGTGCTTCAATTACCAAGGAAGATCAGCAGAGTCTAAACTGAA	6149
	TTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGGTTCTCGTCGGCATT**C**AAGATCCCGTTATTGTTGCCATTTTTGTGTCAAAATCTGTTTCGGCGGTGAGAGAAGAGT	6150
	GGGATCTT**G**AATGCCGA	6151
	TCGGCATT**C**AAGATCCC	6152
Waxy starch GBSS *Pisum sativum* Arg12Term AGA-TGA	ACCGCCGAAACAGATTTTGACACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACG**T**GAACCGCGTGCTTCAATTACCAAGGAAGATCAGCAGAGTCTAAACTGAATTTGCCTCAGA	6153
	TCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGGTTC**A**CGTCGGCATTGAAGATCCCGTTATTGTTGCCATTTTTGTGTCAAAATCTGTTTCGGCGGT	6154
	TGCCGACG**T**GAACCGCG	6155
	CGCGGTTC**A**CGTCGGCA	6156
Waxy starch GBSS *Pisum sativum* Cys15Term TGC-TGA	AGATTTTGACACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACGAGAACCGCGTG**A**TTCAATTACCAAGGAAGATCAGCAGAGTCTAAACTGAATTTGCCTCAGATACACTTCAAT	6157
	ATTGAAGTGTATCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATTGAA**T**CACGCGGTTCTCGTCGGCATTGAAGATCCCGTTATTGTTGCCATTTTTGTGTCAAAATCT	6158
	ACCGCGTG**A**TTCAATTA	6159
	TAATTGAA**T**CACGCGGT	6160
Waxy starch GBSS *Pisum sativum* Tyr18Term TAC-TAG	CACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACGAGAACCGCGTGCTTCAATTA**G**CAAGGAAGATCAGCAGAGTCTAAACTGAATTTGCCTCAGATACACTTCAATAACAACCAA	6161
	TTGGTTGTTATTGAAGTGTATCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTTCCTTG**C**TAATTGAAGCACGCGGTTCTCGTCGGCATTGAAGATCCCGTTATTGTTGCCATTTTTGTG	6162
	TTCAATTA**G**CAAGGAAG	6163
	CTTCCTTG**C**TAATTGAA	6164
Waxy starch GBSS *Manihot esculenta* Ser14Term TCA-TGA	TCTACACCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTCGTTTCCAGGAGCT**G**ACACTTGAGCATCCATGCATTAGAGACTAAGGCTAATAATTTGTCTCACACTGGACCCTG	6165
	CAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTAATGCATGGATGCTCAAGTGT**C**AGCTCCTGGAAACGAAATGTGCAGCTATTACAGTTGCCATGGTGCTCTCTCCGGTGTAGA	6166

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAGGAGCT**G**ACACTTGA	6167
	TCAAGTGT**C**AGCTCCTG	6168
Waxy starch GBSS *Manihot esculenta* Leu16Term TTG-TAG	CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACT**A**GAGCATCCATGCATTAGAGACTAAGGCTAATAATTTGTCTCACACTGGACCCTGGACCCA	6169
	TGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTAATGCATGGATGCTC**T**AGTGTGAGCTCCTGGAAACGAAATGTGCAGCTATTACAGTTGCCATGGTGCTCTCTCCGG	6170
	CTCACACT**A**GAGCATCC	6171
	GGATGCTC**T**AGTGTGAG	6172
Waxy starch GBSS *Manihot esculenta* Leu21Term TTA-TGA	TGGCAACTGTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACTTGAGCATCCATGCAT**G**AGAGACTAAGGCTAATAATTTGTCTCACACTGGACCCTGGACCCAAACTATCACTCCCAA	6173
	TTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCT**C**ATGCATGGATGCTCAAGTGTGAGCTCCTGGAAACGAAATGTGCAGCTATTACAGTTGCCA	6174
	CCATGCAT**G**AGAGACTA	6175
	TAGTCTCT**C**ATGCATGG	6176
Waxy starch GBSS *Manihot esculenta* Glu22Term GAG-TAG	GCAACTGTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACTTGAGCATCCATGCATTA**T**AGACTAAGGCTAATAATTTGTCTCACACTGGACCCTGGACCCAAACTATCACTCCCAATG	6177
	CATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCT**A**TAATGCATGGATGCTCAAGTGTGAGCTCCTGGAAACGAAATGTGCAGCTATTACAGTTGC	6178
	ATGCATTA**T**AGACTAAG	6179
	CTTAGTCT**A**TAATGCAT	6180
Waxy starch GBSS *Manihot esculenta* Lys24Term AAG-TAG	GTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACTTGAGCATCCATGCATTAGAGACT**T**AGGCTAATAATTTGTCTCACACTGGACCCTGGACCCAAACTATCACTCCCAATGGTTTAA	6181
	TTAAACCATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCT**A**AGTCTCTAATGCATGGATGCTCAAGTGTGAGCTCCTGGAAACGAAATGTGCAGCTATTAC	6182
	TAGAGACT**T**AGGCTAAT	6183
	ATTAGCCT**A**AGTCTCTA	6184

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Phaseolus vulgaris* Ser12Term TCA-TGA	ACAACTCCTCCGTCACCGGTATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGCGT**G**AAAAGGCGCGTGGAGTACAGAGACAAAAGTGAAATCTTCGGGTCAGATGAGCCTGAACCG	6185
	CGGTTCAGGCTCATCTGACCCGAAGATTTCACTTTTGTCTCTGTACTCCACGCGCCTTTT**C**ACGCCACGCACGATGCCATCGATACCGTTGCCATGCTTATACCGGTGACGGAGGAGTTGT	6186
	CGTGGCGT**G**AAAAGGCG	6187
	CGCCTTTT**C**ACGCCACG	6188
Waxy starch GBSS *Phaseolus vulgaris* Trp16Term TGG-TGA	CACCGGTATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTG**A**AGTACAGAGACAAAAGTGAAATCTTCGGGTCAGATGAGCCTGAACCGTCATGAATTGAAA	6189
	TTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATTTCACTTTTGTCTCTGTACT**T**CACGCGCCTTTTGACGCCACGCACGATGCCATCGATACCGTTGCCATGCTTATACCGGTG	6190
	GGCGCGTG**A**AGTACAGA	6191
	TCTGTACT**T**CACGCGCC	6192
Waxy starch GBSS *Phaseolus vulgaris* Glu19Term GAG-TAG	ATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTGGAGTACA**T**AGACAAAAGTGAAATCTTCGGGTCAGATGAGCCTGAACCGTCATGAATTGAAATACGATG	6193
	CATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATTTCACTTTTGTCT**A**TGTACTCCACGCGCCTTTTGACGCCACGCACGATGCCATCGATACCGTTGCCATGCTTAT	6194
	GGAGTACA**T**AGACAAAA	6195
	TTTTGTCT**A**TGTACTCC	6196
Waxy starch GBSS *Phaseolus vulgaris* Lys21Term AAA-TAA	ATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTGGAGTACAGAGACA**T**AAGTGAAATCTTCGGGTCAGATGAGCCTGAACCGTCATGAATTGAAATACGATGGGTTGA	6197
	TCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATTTCACTT**A**TGTCTCTGTACTCCACGCGCCTTTTGACGCCACGCACGATGCCATCGATACCGTTGCCAT	6198
	CAGAGACA**T**AAGTGAAA	6199
	TTTCACTT**A**TGTCTCTG	6200
Waxy starch GBSS *Phaseolus vulgaris* Lys23Term AAA-TAA	ACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTGGAGTACAGAGACAAAAGTG**T**AATCTTCGGGTCAGATGAGCCTGAACCGTCATGAATTGAAATACGATGGGTTGAGATCTC	6201
	GAGATCTCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATT**A**CACTTTTGTCTCTGTACTCCACGCGCCTTTTGACGCCACGCACGATGCCATCGATACCGT	6202

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAAAAGTG**T**AATCTTCG	6203
	CGAAGATT**A**CACTTTTG	6204
Waxy starch GBSS *Triticum aestivum* Tyr7Term TAT-TAG	GCGCCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCCTAATTA**G**TGTTCTTATCAAACAAACAGTGTTGGTTCACTGAAACTGTCGCCTCACATCCAATTCCAG	6205
	CTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACTGTTTGTTTGATAAGAACA**C**TAATTAGGAATGGAACCCATTGGTGCAGCCTCTCAATGACGACCTTTTCGAGCTAGGCGC	6206
	CCTAATTA**G**TGTTCTTA	6207
	TAAGAACA**C**TAATTAGG	6208
Waxy starch GBSS *Triticum aestivum* Cys8Term TGT-TGA	CCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCCTAATTATTG**A**TCTTATCAAACAAACAGTGTTGGTTCACTGAAACTGTCGCCTCACATCCAATTCCAGCAA	6209
	TTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACTGTTTGTTTGATAAGA**T**CAATAATTAGGAATGGAACCCATTGGTGCAGCCTCTCAATGACGACCTTTTCGAGCTAGG	6210
	AATTATTG**A**TCTTATCA	6211
	TGATAAGA**T**CAATAATT	6212
Waxy starch GBSS *Triticum aestivum* Tyr10Term TAT-TAG	TCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCCTAATTATTGTTCTTA**G**CAAACAAACAGTGTTGGTTCACTGAAACTGTCGCCTCACATCCAATTCCAGCAATCTTGT	6213
	ACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACTGTTTGTTTG**C**TAAGAACAATAATTAGGAATGGAACCCATTGGTGCAGCCTCTCAATGACGACCTTTTCGA	6214
	TGTTCTTA**G**CAAACAAA	6215
	TTTGTTTG**C**TAAGAACA	6216
Waxy starch GBSS *Triticum aestivum* Gln11Term CAA-TAA	CGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCCTAATTATTGTTCTTAT**T**AAACAAACAGTGTTGGTTCACTGAAACTGTCGCCTCACATCCAATTCCAGCAATCTTGTA	6217
	TACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACTGTTTGTTT**A**ATAAGAACAATAATTAGGAATGGAACCCATTGGTGCAGCCTCTCAATGACGACCTTTTCG	6218
	GTTCTTAT**T**AAACAAAC	6219
	GTTTGTTT**A**ATAAGAAC	6220

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Triticum aestivum* Ser17Term TCA-TGA	AGGCTGCACCAATGGTTCCATTCCTAATTATTGTTCTTATCAAACAAACAGTGTTGGTT**G**ACTGAAACTGTCGCCTCACATCCAATTCCAGCAATCTTGTAACAATGAAGTTATGTTCCT	6221
	AGGAACATAACTTCATTGTTACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGT**C**AACCAACACTGTTTGTTTGATAAGAACAATAATTAGGAATGGAACCCATTGGTGCAGCCT	6222
	TGTTGGTT**G**ACTGAAAC	6223
	GTTTCAGT**C**AACCAACA	6224
Waxy starch GBSS *Triticum aestivum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTTCCGGCGTGCAGGTTTC**T**AGGGCGTGAGGCCCCGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTA	6225
	TAGCTCCGACGGTCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCGGGGCCTCACGCCCT**A**GAAACCTGCACGCCGGAACCTGTCGGTGATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6226
	CAGGTTTC**T**AGGGCGTG	6227
	CACGCCCT**A**GAAACCTG	6228
Waxy starch GBSS *Triticum aestivum* Gly46Term GGA-TGA	GGTTTCCAGGGCGTGAGGCCCCGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTC**T**GAGCTAGCGCCGCCCCAACGCAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCT	6229
	AGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGCGTTGGGGCGGCGCTAGCTC**A**GACGGTCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	6230
	GGACCGTC**T**GAGCTAGC	6231
	GCTAGCTC**A**GACGGTCC	6232
Waxy starch GBSS *Triticum aestivum* Gln53Term CAA-TAA	CGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTAGCGCCGCCCCAACG**T**AAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACCG	6233
	CGGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTT**A**CGTTGGGGCGGCGCTAGCTCCGACGGTCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCG	6234
	CCCCAACG**T**AAAGCCGG	6235
	CCGGCTTT**A**CGTTGGGG	6236
Waxy starch GBSS *Triticum aestivum* Lys56Term AAA-TAA	GCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTAGCGCCGCCCCAACGCAAAGCCGG**T**AAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCG	6237
	CGCCGCTGCCGGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTT**A**CCGGCTTTGCGTTGGGGCGGCGCTAGCTCCGACGGTCCTCATGCCGAGAGCCGCATCCGC	6238

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAGCCGG**T**AAGCGCAC	6239
	GTGCGCTT**A**CCGGCTTT	6240
Waxy starch GBSS *Triticum aestivum* Glu85Term GAG-TAG	CTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCGGCATGAACCT CGTGTTCGTCGGCGCC**T**AGATGGCGCCCTGGAGCAAGACCGGCG GCCTCGGCGACGTCCTCGGGGGCCTCCCCCCAG	6241
	CTGGGGGGAGGCCCCCGAGGACGTCGCCGAGGCCGCCGGTCTT GCTCCAGGGCGCCATCT**A**GGCGCCGACGAACACGAGGTTCATGC CGCCGCTGCCGGTGGCGCGCACCACCATGGAGAG	6242
	TCGGCGCC**T**AGATGGCG	6243
	CGCCATCT**A**GGCGCCGA	6244
Waxy starch GBSS *Triticum aestivum* Gln8Term CAG-TAG	GTCGTCTCTCGCTGCAGGTAGCCACACCCTGCGCGCGCGATGGC GGCTCTGGTCACGTCG**T**AGCTCGCCACCTCCGGCACCGTCCTCG GCATCACCGACAGGTTCCGGCGTGCAGGTTTTC	6245
	GAAAACCTGCACGCCGGAACCTGTCGGTGATGCCGAGGACGGTG CCGGAGGTGGCGAGCT**A**CGACGTGACCAGAGCCGCCATCGCGC GCGCAGGGTGTGGCTACCTGCAGCGAGAGACGAC	6246
	TCACGTCG**T**AGCTCGCC	6247
	GGCGAGCT**A**CGACGTGA	6248
Waxy starch GBSS *Triticum aestivum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTT**T**AGGGTGTGAGGCCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6249
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACACCCT**A**AAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6250
	CAGGTTTT**T**AGGGTGTG	6251
	CACACCCT**A**AAAACCTG	6252
Waxy starch GBSS *Triticum aestivum* Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCG GAGCGAGCGCCGCCCCG**T**AGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG	6253
	CGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCT**A**CGGGGCGGCGCTCGCTCCGGTAGTCC TCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6254
	CCGCCCCG**T**AGCAACAA	6255
	TTGTTGCT**A**CGGGGCGG	6256

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Triticum aestivum* Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCCGAAG**T**AACAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6257
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTT**A**CTTCGGGGCGGCGCTCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6258
	CCCCGAAG**T**AACAAAGC	6259
	GCTTTGTT**A**CTTCGGGG	6260
Waxy starch GBSS *Triticum aestivum* Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCCGAAGCAA**T**AAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6261
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTT**A**TTGCTTCGGGGCGGCGCTCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6262
	CGAAGCAA**T**AAAGCCGG	6263
	CCGGCTTT**A**TTGCTTCG	6264
Waxy starch GBSS *Triticum durum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTTCCGGCGTGCAGGTTTC**T**AGGGCGTGAGGCCCCGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGA	6265
	TCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGCCGGGTTCCGGGGCCTCACGCCCT**A**GAAACCTGCACGCCGGAACCTGTCGGTGATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6266
	CAGGTTTC**T**AGGGCGTG	6267
	CACGCCCT**A**GAAACCTG	6268
Waxy starch GBSS *Triticum durum* Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGCCCCG**T**AGCAAAGCCGGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6269
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTTGCT**A**CGGGGCGGCGCTCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGCCGGGTTCCGGGG	6270
	CCGCCCCG**T**AGCAAAGC	6271
	GCTTTGCT**A**CGGGGCGG	6272
Waxy starch GBSS *Triticum durum* Gln53Term CAA-TAA	CGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGCCCCGAAG**T**AAAGCCGGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6273
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTT**A**CTTCGGGGCGGCGCTCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGCCGGGTTCCG	6274

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCCCGAAG**T**AAAGCCGG	6275
	CCGGCTTT**A**CTTCGGGG	6276
Waxy starch GBSS *Triticum durum* Lys56Term AAA-TAA	GCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGCCCCGAAGCAAAGCCGG**T**AAGCGCACCGCGGGAGCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGGGCAGCGGCG	6277
	CGCCGCTGCCCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGCTCCCGCGGTGCGCTT**A**CCGGCTTTGCTTCGGGGCGGCGCTCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGC	6278
	AAAGCCGG**T**AAGCGCAC	6279
	GTGCGCTT**A**CCGGCTTT	6280
Waxy starch GBSS *Triticum durum* Cys64Term TGC-TGA	TATCGGAGCGAGCGCCGCCCCGAAGCAAAGCCGGAAAGCGCACCGCGGGAGCCGGCGGTG**A**CTCTCCATGGTGGTGCGCGCCACGGGCAGCGGCGGCATGAACCTCGTGTTCGTCGGCGCC	6281
	GGCGCCGACGAACACGAGGTTCATGCCGCCGCTGCCCGTGGCGCGCACCACCATGGAGAG**T**CACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTTGCTTCGGGGCGGCGCTCGCTCCGATA	6282
	CGGCGGTG**A**CTCTCCAT	6283
	ATGGAGAG**T**CACCGCCG	6284
Waxy starch GBSS *Triticum turgidum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTTCCGGCGTGCAGGTTTT**T**AGGGTGTGAGGCCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6285
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGGCCTCACACCCT**A**AAAACCTGCACGCCGGAACCTGTCGGTGATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6286
	CAGGTTTT**T**AGGGTGTG	6287
	CACACCCT**A**AAAACCTG	6288
Waxy starch GBSS *Triticum turgidum* Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCCG**T**AGCAACAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG	6289
	CGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTGCT**A**CGGGGCGGCGCTCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6290
	CCGCCCCG**T**AGCAACAA	6291
	TTGTTGCT**A**CGGGGCGG	6292

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Triticum turgidum* Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCCGAAG**T**AACAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6293
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTT**A**CTTCGGGGCGGCGCTCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6294
	CCCCGAAG**T**AACAAAGC	6295
	GCTTTGTT**A**CTTCGGGG	6296
Waxy starch GBSS *Triticum turgidum* Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCCGAAGCAA**T**AAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6297
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTT**A**TTGCTTCGGGGCGGCGCTCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6298
	CGAAGCAA**T**AAAGCCGG	6299
	CCGGCTTT**A**TTGCTTCG	6300
Waxy starch GBSS *Triticum turgidum* Lys57Term AAA-TAA	GATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCCGAAGCAACAAAGCCGG**T**AAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGGGCAGCGCCG	6301
	CGGCGCTGCCCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTT**A**CCGGCTTTGTTGCTTCGGGGCGGCGCTCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATC	6302
	AAAGCCGG**T**AAGCGCAC	6303
	GTGCGCTT**A**CCGGCTTT	6304
Waxy starch GBSS *Aegilops speltoides* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGCCACCGTCCTCGGCATCACCGACAGGTTCCGCCATGCAGGTTTC**T**AGGGCGTGAGGCCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAGCGA	6305
	TCGCTCCGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGGCCTCACGCCCT**A**GAAACCTGCATGGCGGAACCTGTCGGTGATGCCGAGGACGGTGGCGGAGGTGGCGAGCTG	6306
	CAGGTTTC**T**AGGGCGTG	6307
	CACGCCCT**A**GAAACCTG	6308
Waxy starch GBSS *Aegilops speltoides* Gly46Term GGA-TGA	GGTTTCCAGGGCGTGAGGCCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTC**T**GAGCGAGCGCCGCCCCGAAGCAACAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCC	6309
	GGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTGCTTCGGGGCGGCGCTCGCTC**A**GACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	6310

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGACTGTCTGAGCGAGC	6311
	GCTCGCTCAGACAGTCC	6312
Waxy starch GBSS *Aegilops speltoides* Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCG GAGCGAGCGCCGCCCCGTAGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCGATGGTGGTGCGCG	6313
	CGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCTACGGGGCGGCGCTCGCTCCGACAGTCC TCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6314
	CCGCCCCGTAGCAACAA	6315
	TTGTTGCTACGGGGCGG	6316
Waxy starch GBSS *Aegilops speltoides* Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAG CGAGCGCCGCCCCGAAGTAACAAAGCCGGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCGATGGTGGTGCGCGCCA	6317
	TGGCGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGACAG TCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6318
	CCCCGAAGTAACAAAGC	6319
	GCTTTGTTACTTCGGGG	6320
Waxy starch GBSS *Aegilops speltoides* Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAGCGA GCGCCGCCCCGAAGCAATAAAGCCGGAAAGCGCACCGCGGGAC CCGGCGGTGCCTCTCGATGGTGGTGCGCGCCACCG	6321
	CGGTGGCGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGA CAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6322
	CGAAGCAATAAAGCCGG	6323
	CCGGCTTTATTGCTTCG	6324
Waxy starch GBSS *Oryza glaberrima* Gln8Term CAG-TAG	AGTGCAGAGATCTTCCACAGCAACAGCTAGACAACCACCATGTCG GCTCTCACCACGTCCTAGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCTGACAGGTCGGCGCCGTCGTCGCTGC	6325
	GCAGCGACGACGGCGCCGACCTGTCAGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG GTTGTCTAGCTGTTGCTGTGGAAGATCTCTGCACT	6326
	CCACGTCCTAGCTCGCC	6327
	GGCGAGCTAGGACGTGG	6328

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Oryza glaberrima* Ser12Term TCG-TAG	TCCACAGCAACAGCTAGACAACCACCATGTCGGCTCTCACCACGT CCCAGCTCGCCACCTAGGCCACCGGCTTCGGCATCGCTGACAGG TCGGCGCCGTCGTCGCTGCTCCGCCACGGGTT	6329
	AACCCGTGGCGGAGCAGCGACGACGGCGCCGACCTGTCAGCGAT GCCGAAGCCGGTGGCCTAGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGA	6330
	CGCCACCTAGGCCACCG	6331
	CGGTGGCCTAGGTGGCG	6332
Waxy starch GBSS *Oryza glaberrima* Ser22Term TCG-TAG	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCTGACAGGTAGGCGCCGTCGTCGCTGCTCCGCCACGG GTTCCAGGGCCTCAAGCCCCGCAGCCCCGCCGG	6333
	CCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACCCGTGGCGGA GCAGCGACGACGGCGCCTACCTGTCAGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6334
	TGACAGGTAGGCGCCGT	6335
	ACGGCGCCTACCTGTCA	6336
Waxy starch GBSS *Oryza glaberrima* Ser25Term TCG-TAG	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCT GACAGGTCGGCGCCGTAGTCGCTGCTCCGCCACGGGTTCCAGG GCCTCAAGCCCCGCAGCCCCGCCGGCGGCGACGC	6337
	GCGTCGCCGCCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACC CGTGGCGGAGCAGCGACTACGGCGCCGACCTGTCAGCGATGCC GAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	6338
	GGCGCCGTAGTCGCTGC	6339
	GCAGCGACTACGGCGCC	6340
Waxy starch GBSS *Oryza glaberrima* Ser26Term TCG-TAG	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCTGAC AGGTCGGCGCCGTCGTAGCTGCTCCGCCACGGGTTCCAGGGCCT CAAGCCCCGCAGCCCCGCCGGCGGCGACGCGAC	6341
	GTCGCGTCGCCGCCGGCGGGGCTGCGGGGCTTGAGGCCCTGGA ACCCGTGGCGGAGCAGCTACGACGGCGCCGACCTGTCAGCGATG CCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	6342
	GCCGTCGTAGCTGCTCC	6343
	GGAGCAGCTACGACGGC	6344
Waxy starch GBSS *Oryza sativa* Gln8Term CAG-TAG	TCCACAGCAAGAGCTAAACAGCCGACCGTGTGCACCACCATGTCG GCTCTCACCACGTCCTAGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCCGACAGGTCGGCGCCGTCGTCGCTGC	6345
	GCAGCGACGACGGCGCCGACCTGTCGGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG GTGCACACGGTCGGCTGTTTAGCTCTTGCTGTGGA	6346

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCACGTCC**T**AGCTCGCC	6347
	GGCGAGCT**A**GGACGTGG	6348
Waxy starch GBSS *Oryza sativa* Ser12Term TCG-TAG	CTAAACAGCCGACCGTGTGCACCACCATGTCGGCTCTCACCACGT CCCAGCTCGCCACCT**A**GGCCACCGGCTTCGGCATCGCCGACAGG TCGGCGCCGTCGTCGCTGCTTCGCCACGGGTT	6349
	AACCCGTGGCGAAGCAGCGACGACGGCGCCGACCTGTCGGCGAT GCCGAAGCCGGTGGCC**T**AGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTGCACACGGTCGGCTGTTTAG	6350
	CGCCACCT**A**GGCCACCG	6351
	CGGTGGCC**T**AGGTGGCG	6352
Waxy starch GBSS *Oryza sativa* Ser22Term TCG-TAG	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCCGACAGGT**A**GGCGCCGTCGTCGCTGCTTCGCCACGG GTTCCAGGGCCTCAAGCCCCGTAGCCCAGCCGG	6353
	CCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCCGTGGCGAA GCAGCGACGACGGCGCC**T**ACCTGTCGGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6354
	CGACAGGT**A**GGCGCCGT	6355
	ACGGCGCC**T**ACCTGTCG	6356
Waxy starch GBSS *Oryza sativa* Ser25Term TCG-TAG	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCC GACAGGTCGGCGCCGT**A**GTCGCTGCTTCGCCACGGGTTCCAGGG CCTCAAGCCCCGTAGCCCAGCCGGCGGGGACGC	6357
	GCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACC CGTGGCGAAGCAGCGAC**T**ACGGCGCCGACCTGTCGGCGATGCC GAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	6358
	GGCGCCGT**A**GTCGCTGC	6359
	GCAGCGAC**T**ACGGCGCC	6360
Waxy starch GBSS *Oryza sativa* Ser26Term TCG-TAG	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCCGAC AGGTCGGCGCCGTCGT**A**GCTGCTTCGCCACGGGTTCCAGGGCCT CAAGCCCCGTAGCCCAGCCGGCGGGGACGCATC	6361
	GATGCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAA CCCGTGGCGAAGCAGC**T**ACGACGGCGCCGACCTGTCGGCGATGC CGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	6362
	GCCGTCGT**A**GCTGCTTC	6363
	GAAGCAGC**T**ACGACGGC	6364

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Hordeum vulgare* Gln8Term CAG-TAG	GTCTCTCACTGCAGGTAGCCACACCCTGTGCGCGGCGCCATGGCGGCTCTGGCCACGTCC**T**AGCTCGCCACCTCCGGCACCGTCCTCGGCGTCACCGACAGATTCCGGCGTCCAGGTTTTC	6365
	GAAAACCTGGACGCCGGAATCTGTCGGTGACGCCGAGGACGGTGCCGGAGGTGGCGAGCT**A**GGACGTGGCCAGAGCCGCCATGGCGCCGCGCACAGGGTGTGGCTACCTGCAGTGAGAGAC	6366
	CCACGTCC**T**AGCTCGCC	6367
	GGCGAGCT**A**GGACGTGG	6368
Waxy starch GBSS *Hordeum vulgare* Arg21Term AGA-TGA	ATGGCGGCTCTGGCCACGTCCCAGCTCGCCACCTCCGGCACCGTCCTCGGCGTCACCGAC**T**GATTCCGGCGTCCAGGTTTTCAGGGCCTCAGGCCCCGGAACCCGGCGGATGCGGCGCTTG	6369
	CAAGCGCCGCATCCGCCGGGTTCCGGGGCCTGAGGCCCTGAAAACCTGGACGCCGGAATC**A**GTCGGTGACGCCGAGGACGGTGCCGGAGGTGGCGAGCTGGGACGTGGCCAGAGCCGCCAT	6370
	TCACCGAC**T**GATTCCGG	6371
	CCGGAATC**A**GTCGGTGA	6372
Waxy starch GBSS *Hordeum vulgare* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCGTCACCGACAGATTCCGGCGTCCAGGTTTT**T**AGGGCCTCAGGCCCCGGAACCCGGCGGATGCGGCGCTTGGTATGAGGACTATCGGAGCAA	6373
	TTGCTCCGATAGTCCTCATACCAAGCGCCGCATCCGCCGGGTTCCGGGGCCTGAGGCCCT**A**AAAACCTGGACGCCGGAATCTGTCGGTGACGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6374
	CAGGTTTT**T**AGGGCCTC	6375
	GAGGCCCT**A**AAAACCTG	6376
Waxy starch GBSS *Hordeum vulgare* Gly46Term GGA-TGA	GGTTTTCAGGGCCTCAGGCCCCGGAACCCGGCGGATGCGGCGCTTGGTATGAGGACTATC**T**GAGCAAGCGCCGCCCCGAAGCAAAGCCGGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCT	6377
	AGAGGCACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTTGCTTCGGGGCGGCGCTTGCTC**A**GATAGTCCTCATACCAAGCGCCGCATCCGCCGGGTTCCGGGGCCTGAGGCCCTGAAAACC	6378
	GGACTATC**T**GAGCAAGC	6379
	GCTTGCTC**A**GATAGTCC	6380
Waxy starch GBSS *Hordeum vulgare* Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCGGCGCTTGGTATGAGGACTATCGGAGCAAGCGCCGCCCCG**T**AGCAAAGCCGGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCTCCGTGGTGGTGAGCGCCA	6381
	TGGCGCTCACCACCACGGAGAGGCACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTTGCT**A**CGGGGCGGCGCTTGCTCCGATAGTCCTCATACCAAGCGCCGCATCCGCCGGGTTCCGGGG	6382

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGCCCCG**T**AGCAAAGC	6383
	GCTTTGCT**A**CGGGGCGG	6384
Waxy starch GBSS *Zea mays* Gln8Term CAG-TAG	ACGTCTTTTCTCTCTCTCCTACGCAGTGGATTAATCGGCATGGCGGCTCTGGCCACGTCG**T**AGCTCGTCGCAACGCGCGCCGGCCTGGGCGTCCCGGACGCGTCCACGTTCCGCCGCGGCG	6385
	CGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCCAGGCCGGCGCGCGTTGCGACGAGCT**A**CGACGTGGCCAGAGCCGCCATGCCGATTAATCCACTGCGTAGGAGAGAGAGAAAAGACGT	6386
	CCACGTCG**T**AGCTCGTC	6387
	GACGAGCT**A**CGACGTGG	6388
Waxy starch GBSS *Zea mays* Gln30Term CAG-TAG	GTCGCAACGCGCGCCGGCCTGGGCGTCCCGGACGCGTCCACGTTCCGCCGCGGCGCCGCG**T**AGGGCCTGAGGGGGGCCCGGGCGTCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCG	6389
	CGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGACGCCCGGGCCCCCCTCAGGCCCT**A**CGCGGCGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCCAGGCCGGCGCGCGTTGCGAC	6390
	GCGCCGCG**T**AGGGCCTG	6391
	CAGGCCCT**A**CGCGGCGC	6392
Waxy starch GBSS *Zea mays* Ser38Term TCG-TAG	TCCCGGACGCGTCCACGTTCCGCCGCGGCGCCGCGCAGGGCCTGAGGGGGGCCCGGGCGT**A**GGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCGCGGCGCCCAGGCACCAGCA	6393
	TGCTGGTGCCTGGGCGCCGCGCGCGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGCC**T**ACGCCCGGGCCCCCCTCAGGCCCTGCGCGGCGCCGCGGCGGAACGTGGACGCGTCCGGGA	6394
	CCGGGCGT**A**GGCGGCGG	6395
	CCGCCGCC**T**ACGCCCGG	6396
Waxy starch GBSS *Zea mays* Ser57Term CAG-TAG	GCGTCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCGCGGCGCCCAGGCAC**T**AGCAGCAGGCGCGCCGCGGGGGCAGGTTCCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCA	6397
	TGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCCCCGCGGCGCGCCTGCTGCT**A**GTGCCTGGGCGCCGCGCGCGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGACGC	6398
	CCAGGCAC**T**AGCAGCAG	6399
	CTGCTGCT**A**GTGCCTGG	6400

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Zea mays* Gln58Term CAG-TAG	TCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCG CGGCGCCCAGGCACCAG**T**AGCAGGCGCGCCGCGGGGGCAGGTT CCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCATGA	6401
	TCATGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCC CCGCGGCGCGCCTGCT**A**CTGGTGCCTGGGCGCCGCGCGCGCGC TGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGA	6402
	GGCACCAG**T**AGCAGGCG	6403
	CGCCTGCT**A**CTGGTGCC	6404

Example 11

Altering fatty acid content of plants

Improved means to manipulate fatty acid compositions, from biosynthetic or natural plant sources, are needed. For example, oils containing reduced saturated fatty acids are desired for dietary reasons and oils containing increased saturated fatty acids are also needed as alternatives to current sources of highly saturated oil products, such as tropical oils or chemically hydrogenated oils. It would therefore be advantageous to influence directly the production and composition of fatty acids in crop plants.

Higher plants synthesize fatty acids, primarily palmitic, stearic and oleic acids, in the plastids (i.e., chloroplasts, proplastids, or other related organelles) as part of the Fatty Acid Synthase (FAS) complex. Fatty acid synthesis is the result of the three enzymatic activities: acyl-ACP elongase, acyl-ACP desaturase and acyl-ACP thioesterases specific for each of palmitoyl-, stearoyl- and oleoyl-ACP.

A variety of enzymes have been identified that influence the relative levels of saturated vs. unsaturated fatty acids in plants. For example, the enzymes stearoyl-acyl carrier protein (stearoyl-ACP) desaturase, oleoyl desaturase and linoleate desaturase produce unsaturated fatty acids from saturated precursors. Similarly, relative enzymatic activities of the various acyl-ACP thioesterases influences the relative acyl-chain composition of the resultant fatty acids. Consequently a reduction or an increase of the activity of these enzymes can alter the properties of oils produced in a plant. In fact, specific targeting of particular enzymatic activities can results in altered levels of particular fatty acids.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes encoding proteins involved in fatty acid biosynthesis.

Table 22
Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Ser8Term TCG-TAG	TTTGGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGC CACCTCTGCTACGT<u>A</u>GTCATTCTTTCCTGTACCATCTTCTTCACTT GATCCTAATGGAAAAGGCAATAAGATTGG	6405
	CCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATGGTA CAGGAAAGAATGAC<u>T</u>ACGTAGCAGAGGTGGCCACCATGACGAGG AGATGAAGCGTTCAAAGACACTGCCACCAAA	6406

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCTACGT**A**GTCATTCT	6407
	AGAATGAC**T**ACGTAGCA	6408
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Ser9Term TCA-TGA	GGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGCCACCTCTGCTACGTCGT**G**ATTCTTTCCTGTACCATCTTCTTCACTTGATCCTAATGGAAAAGGCAATAAGATTGGGTC	6409
	GACCCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATGGTACAGGAAAGAAT**C**ACGACGTAGCAGAGGTGGCCACCATGACGAGGAGATGAAGCGTTCAAAGACACTGCCACC	6410
	TACGTCGT**G**ATTCTTTC	6411
	GAAAGAAT**C**ACGACGTA	6412
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Ser17Term TCA-TGA	ATCTCCTCGTCATGGTGGCCACCTCTGCTACGTCGTCATTCTTTCCTGTACCATCTTCTT**G**ACTTGATCCTAATGGAAAAGGCAATAAGATTGGGTCTACGAATCTTGCTGGACTCAATTC	6413
	GAATTGAGTCCAGCAAGATTCGTAGACCCAATCTTATTGCCTTTTCCATTAGGATCAAGT**C**AAGAAGATGGTACAGGAAAGAATGACGACGTAGCAGAGGTGGCCACCATGACGAGGAGAT	6414
	ATCTTCTT**G**ACTTGATC	6415
	GATCAAGT**C**AAGAAGAT	6416
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Gly22Term GGA-TGA	GTGGCCACCTCTGCTACGTCGTCATTCTTTCCTGTACCATCTTCTTCACTTGATCCTAAT**T**GAAAAGGCAATAAGATTGGGTCTACGAATCTTGCTGGACTCAATTCTGCACCTAACTCTG	6417
	CAGAGTTAGGTGCAGAATTGAGTCCAGCAAGATTCGTAGACCCAATCTTATTGCCTTTTC**A**ATTAGGATCAAGTGAAGAAGATGGTACAGGAAAGAATGACGACGTAGCAGAGGTGGCCAC	6418
	ATCCTAAT**T**GAAAAGGC	6419
	GCCTTTTC**A**ATTAGGAT	6420
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Ser8Term TCA-TGA	GCTTGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGT**G**ATCATTCTTTCCGTTGACTTCCCCTTCTGGGGATGCCAAATCGGGCAATCCCGGAAAAGG	6421
	CCTTTTCCGGGATTGCCCGATTTGGCATCCCCAGAAGGGGAAGTCAACGGAAAGAATGAT**C**ACGTGGCGGCAGTAGCAACCATTGTGGCCACAATTAACCAATCAGATCACAAATTCAAGC	6422
	CGCCACGT**G**ATCATTCT	6423
	AGAATGAT**C**ACGTGGCG	6424

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Ser9Term TCA-TGA	TGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGTCAT**G**ATTCTTTCCGTTGACTTCCCCTTCTGGGGATGCCAAATCGGGCAATCCCGGAAAAGGGTC	6425
	GACCCTTTTCCGGGATTGCCCGATTTGGCATCCCCAGAAGGGGAAGTCAACGGAAAGAAT**C**ATGACGTGGCGGCAGTAGCAACCATTGTGGCCACAATTAACCAATCAGATCACAAATTCA	6426
	CACGTCAT**G**ATTCTTTC	6427
	GAAAGAAT**C**ATGACGTG	6428
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Leu13Term TTG-TAG	CTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGTCATCATTCTTTCCGT**A**GACTTCCCCTTCTGGGGATGCCAAATCGGGCAATCCCGGAAAAGGGTCGGTGAGTTTTGG	6429
	CCAAAACTCACCGACCCTTTTCCGGGATTGCCCGATTTGGCATCCCCAGAAGGGGAAGTC**T**ACGGAAAGAATGATGACGTGGCGGCAGTAGCAACCATTGTGGCCACAATTAACCAATCAG	6430
	CTTTCCGT**A**GACTTCCC	6431
	GGGAAGTC**T**ACGGAAAG	6432
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Lys21Term AAA-TAA	ATGGTTGCTACTGCCGCCACGTCATCATTCTTTCCGTTGACTTCCCCTTCTGGGGATGCC**T**AATCGGGCAATCCCGGAAAAGGGTCGGTGAGTTTTGGGTCAATGAAGTCGAAATCCGCGG	6433
	CCGCGGATTTCGACTTCATTGACCCAAAACTCACCGACCCTTTTCCGGGATTGCCCGATT**A**GGCATCCCCAGAAGGGGAAGTCAACGGAAAGAATGATGACGTGGCGGCAGTAGCAACCAT	6434
	GGGATGCC**T**AATCGGGC	6435
	GCCCGATT**A**GGCATCCC	6436
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Ser8Term TCG-TAG	GGGATTTCAGCACGAAATTGAAGTTGTTTTTAAAAACCATGGTTGCTACTGCTGTGACAT**A**GGCGTTTTTCCCAGTCACTTCTTCACCTGACTCCTCTGACTCGAAAAACAAGAAGCTCGG	6437
	CCGAGCTTCTTGTTTTTCGAGTCAGAGGAGTCAGGTGAAGAAGTGACTGGGAAAAACGCC**T**ATGTCACAGCAGTAGCAACCATGGTTTTTAAAAACAACTTCAATTTCGTGCTGAAATCCC	6438
	TGTGACAT**A**GGCGTTTT	6439
	AAAACGCC**T**ATGTCACA	6440
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Ser16Term TCA-TGA	TGTTTTTAAAAACCATGGTTGCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTT**G**ACCTGACTCCTCTGACTCGAAAAACAAGAAGCTCGGAAGCATCAAGTCGAAGCCATCGGT	6441
	ACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTTTTCGAGTCAGAGGAGTCAGGT**C**AAGAAGTGACTGGGAAAAACGCCGATGTCACAGCAGTAGCAACCATGGTTTTTAAAAACA	6442

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CACTTCTT**G**ACCTGACT	6443
	AGTCAGGT**C**AAGAAGTG	6444
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Ser22Term TCG-TAG	TTGCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACCTGACTCCTCTGACT**A**GAAAAACAAGAAGCTCGGAAGCATCAAGTCGAAGCCATCGGTTTCTTCTGGAAGTTTGCA	6445
	TGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTTTTC**T**AGTCAGAGGAGTCAGGTGAAGAAGTGACTGGGAAAAACGCCGATGTCACAGCAGTAGCAA	6446
	CTCTGACT**A**GAAAAACA	6447
	TGTTTTTC**T**AGTCAGAG	6448
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Lys23Term AAA-TAA	GCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACCTGACTCCTCTGACTCG**T**AAAACAAGAAGCTCGGAAGCATCAAGTCGAAGCCATCGGTTTCTTCTGGAAGTTTGCAAG	6449
	CTTGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTTT**A**CGAGTCAGAGGAGTCAGGTGAAGAAGTGACTGGGAAAAACGCCGATGTCACAGCAGTAGC	6450
	CTGACTCG**T**AAAACAAG	6451
	CTTGTTTT**A**CGAGTCAG	6452
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Ser14Term TCG-TAG	CTCCCGCTCGTTGAAAGACAATGGTGGCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGT**A**GTCCCCGGTCACCTCCTCTAGACCAGGAAAGCCCGGAAATGGGTCATCGAGCTTCAGCCC	6453
	GGGCTGAAGCTCGATGACCCATTTCCGGGCTTTCCTGGTCTAGAGGAGGTGACCGGGGAC**T**ACACGGGGAAGAATGCAGAGCTTGCAGCGGTAGCCACCATTGTCTTTCAACGAGCGGGAG	6454
	CCCCGTGT**A**GTCCCCGG	6455
	CCGGGGAC**T**ACACGGGG	6456
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Arg21Term AGA-TGA	ATGGTGGCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACCTCCTCT**T**GACCAGGAAAGCCCGGAAATGGGTCATCGAGCTTCAGCCCCATCAAGCCCAAATTTGTCG	6457
	CGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTTCCGGGCTTTCCTGGTC**A**AGAGGAGGTGACCGGGGACGACACGGGGAAGAATGCAGAGCTTGCAGCGGTAGCCACCAT	6458
	CCTCCTCT**T**GACCAGGA	6459
	TCCTGGTC**A**AGAGGAGG	6460

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Gly23Term GGA-TGA	GCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACCTCCTCTAGACCA**T**GAAAGCCCGGAAATGGGTCATCGAGCTTCAGCCCCATCAAGCCCAAATTTGTCGCCAATG	6461
	CATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTTCCGGGCTTTC**A**TGGTCTAGAGGAGGTGACCGGGGACGACACGGGGAAGAATGCAGAGCTTGCAGCGGTAGC	6462
	CTAGACCA**T**GAAAGCCC	6463
	GGGCTTTC**A**TGGTCTAG	6464
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys24Term AAG-TAG	ACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACCTCCTCTAGACCAGGA**T**AGCCCGGAAATGGGTCATCGAGCTTCAGCCCCATCAAGCCCAAATTTGTCGCCAATGGCG	6465
	CGCCATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTTCCGGGCT**A**TCCTGGTCTAGAGGAGGTGACCGGGGACGACACGGGGAAGAATGCAGAGCTTGCAGCGGT	6466
	GACCAGGA**T**AGCCCGGA	6467
	TCCGGGCT**A**TCCTGGTC	6468
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Gly23Term GGA-TGA	GCCACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCG**T**GAAAGCTCGGAAATGGGTCATCGAGCTTGAGCCCCCTCAAGCCCAAATTTGTCGCCAATG	6469
	CATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACCCATTTCCGAGCTTTC**A**CGGCCTAGAGGAGGTGTCCGGGGACGGCAGGGGGAAGAATGCAGAACTTGCAGCGGTGGC	6470
	CTAGGCCG**T**GAAAGCTC	6471
	GAGCTTTC**A**CGGCCTAG	6472
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Lys24Term AAG-TAG	ACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGGA**T**AGCTCGGAAATGGGTCATCGAGCTTGAGCCCCCTCAAGCCCAAATTTGTCGCCAATGCCG	6473
	CGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACCCATTTCCGAGCT**A**TCCCGGCCTAGAGGAGGTGTCCGGGGACGGCAGGGGGAAGAATGCAGAACTTGCAGCGGT	6474
	GGCCGGGA**T**AGCTCGGA	6475
	TCCGAGCT**A**TCCCGGCC	6476
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Gly26Term GGA-TGA	GCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGGAAAGCTC**T**GAAATGGGTCATCGAGCTTGAGCCCCCTCAAGCCCAAATTTGTCGCCAATGCCGGGTTGA	6477
	TCAACCCGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACCCATTTC**A**GAGCTTTCCCGGCCTAGAGGAGGTGTCCGGGACGGCAGGGGGAAGAATGCAGAACTTGC	6478

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAAAGCTC**T**GAAATGGG	6479
	CCCATTTC**A**GAGCTTTC	6480
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Ser29Term TCA-TGA	CATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGGAA AGCTCGGAAATGGGT**G**ATCGAGCTTGAGCCCCCTCAAGCCCAAAT TTGTCGCCAATGCCGGGTTGAAGGTTAAGGC	6481
	GCCTTAACCTTCAACCCGGCATTGGCGACAAATTTGGGCTTGAGG GGGCTCAAGCTCGAT**C**ACCCATTTCCGAGCTTTCCCGGCCTAGAG GAGGTGTCCGGGGACGGCAGGGGGAAGAATG	6482
	AAATGGGT**G**ATCGAGCT	6483
	AGCTCGAT**C**ACCCATTT	6484
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Ser9Term TCG-TAG	CGTTTAAGTGGATCGGACATTTAAGTGTTTTAATCATGGTAGCTAT GAGTGCTACTGCGT**A**GCTGTTTCCGGTTTCTTCCCCAAAACCTCA CTCTGGAGCCAAGACATCTGATAAGCTTGG	6485
	CCAAGCTTATCAGATGTCTTGGCTCCAGAGTGAGGTTTTGGGGAA GAAACCGGAAACAGC**T**ACGCAGTAGCACTCATAGCTACCATGATT AAAACACTTAAATGTCCGATCCACTTAAACG	6486
	TACTGCGT**A**GCTGTTTC	6487
	GAAACAGC**T**ACGCAGTA	6488
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Lys17Term AAA-TAA	AGTGTTTTAATCATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTC CGGTTTCTTCCCCA**T**AACCTCACTCTGGAGCCAAGACATCTGATAA GCTTGGAGGTGAACCAGGTAGTGTTGCTG	6489
	CAGCAACACTACCTGGTTCACCTCCAAGCTTATCAGATGTCTTGGC TCCAGAGTGAGGTT**A**TGGGGAAGAAACCGGAAACAGCGACGCAG TAGCACTCATAGCTACCATGATTAAAACACT	6490
	CTTCCCCA**T**AACCTCAC	6491
	GTGAGGTT**A**TGGGGAAG	6492
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Gly21Term GGA-TGA	ATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCC CAAAACCTCACTCT**T**GAGCCAAGACATCTGATAAGCTTGGAGGTGA ACCAGGTAGTGTTGCTGTGCGCGGAATCA	6493
	TGATTCCGCGCACAGCAACACTACCTGGTTCACCTCCAAGCTTATC AGATGTCTTGGCTC**A**AGAGTGAGGTTTTGGGGAAGAAACCGGAAA CAGCGACGCAGTAGCACTCATAGCTACCAT	6494
	CTCACTCT**T**GAGCCAAG	6495
	CTTGGCTC**A**AGAGTGAG	6496

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Lys23Term AAG-TAG	GCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCCCAAAAC CTCACTCTGGAGCC**T**AGACATCTGATAAGCTTGGAGGTGAACCAG GTAGTGTTGCTGTGCGCGGAATCAAGACAA	6497
	TTGTCTTGATTCCGCGCACAGCAACACTACCTGGTTCACCTCCAAG CTTATCAGATGTCT**A**GGCTCCAGAGTGAGGTTTTGGGGAAGAAAC CGGAAACAGCGACGCAGTAGCACTCATAGC	6498
	CTGGAGCC**T**AGACATCT	6499
	AGATGTCT**A**GGCTCCAG	6500
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Lys21Term AAA-TAA	ATGGTGGCTGCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCC CCAGGAGCCTCCCCT**T**AACCTGGGAAGTTAGGCAACTGGTCATCG AGTTTGAGCCCTTCCTTGAAGCCCAAGTCAA	6501
	TTGACTTGGGCTTCAAGGAAGGGCTCAAACTCGATGACCAGTTGC CTAACTTCCCAGGTT**A**AGGGGAGGCTCCTGGGGATGGAACAGGG AAGCATGCAGAACTTGCTGCAGCAGCCACCAT	6502
	CCTCCCCT**T**AACCTGGG	6503
	CCCAGGTT**A**AGGGGAGG	6504
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Lys24Term AAG-TAG	GCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCCCCAGGAGCC TCCCCTAAACCTGGG**T**AGTTAGGCAACTGGTCATCGAGTTTGAGC CCTTCCTTGAAGCCCAAGTCAATCCCCAATG	6505
	CATTGGGGATTGACTTGGGCTTCAAGGAAGGGCTCAAACTCGATG ACCAGTTGCCTAACT**A**CCCAGGTTTAGGGGAGGCTCCTGGGGATG GAACAGGGAAGCATGCAGAACTTGCTGCAGC	6506
	AACCTGGG**T**AGTTAGGC	6507
	GCCTAACT**A**CCCAGGTT	6508
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Trp28Term TGG-TGA	TGCATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGG GAAGTTAGGCAACTG**A**TCATCGAGTTTGAGCCCTTCCTTGAAGCC CAAGTCAATCCCCAATGGCGGATTTCAGGTT	6509
	AACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAAGG GCTCAAACTCGATGA**T**CAGTTGCCTAACTTCCCAGGTTTAGGGGA GGCTCCTGGGGATGGAACAGGGAAGCATGCA	6510
	GGCAACTG**A**TCATCGAG	6511
	CTCGATGA**T**CAGTTGCC	6512
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Ser29Term TCA-TGA	CATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGGGA AGTTAGGCAACTGGT**G**ATCGAGTTTGAGCCCTTCCTTGAAGCCCA AGTCAATCCCCAATGGCGGATTTCAGGTTAA	6513
	TTAACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAA GGGCTCAAACTCGAT**C**ACCAGTTGCCTAACTTCCCAGGTTTAGGG GAGGCTCCTGGGGATGGAACAGGGAAGCATG	6514

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAACTGGT**G**ATCGAGTT	6515
	AACTCGAT**C**ACCAGTTG	6516
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys21Term AAA-TAA	ATGGTGGCTGCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACCCCGGGAATCTCCCCT**T**AACCCGGGAAGTTCGGTAATGGTGGCTTTCAGGTTAAGGCAAACGCCAATGCCCATCCTA	6517
	TAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGCCACCATTACCGAACTTCCCGGGTT**A**AGGGGAGATTCCCGGGGTTGGAACGGAGAAGAATGCAGAACTTGCTGCGGCAGCCACCAT	6518
	TCTCCCCT**T**AACCCGGG	6519
	CCCGGGTT**A**AGGGGAGA	6520
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys24Term AAG-TAG	GCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACCCCGGGAATCTCCCCTAAACCCGGG**T**AGTTCGGTAATGGTGGCTTTCAGGTTAAGGCAAACGCCAATGCCCATCCTAGTCTAAAGT	6521
	ACTTTAGACTAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGCCACCATTACCGAACT**A**CCCGGGTTTAGGGGAGATTCCCGGGGTTGGAACGGAGAAGAATGCAGAACTTGCTGCGGC	6522
	AACCCGGG**T**AGTTCGGT	6523
	ACCGAACT**A**CCCGGGTT	6524
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Gln31Term CAG-TAG	TTCTCCGTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTCGGTAATGGTGGCTTT**T**AGGTTAAGGCAAACGCCAATGCCCATCCTAGTCTAAAGTCTGGCAGCCTCGAGACTGAAG	6525
	CTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGGCATTGGCGTTTGCCTTAACCT**A**AAAGCCACCATTACCGAACTTCCCGGGTTTAGGGGAGATTCCCGGGGTTGGAACGGAGAA	6526
	GTGGCTTT**T**AGGTTAAG	6527
	CTTAACCT**A**AAAGCCAC	6528
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys33Term AAG-TAG	GTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTCGGTAATGGTGGCTTTCAGGTT**T**AGGCAAACGCCAATGCCCATCCTAGTCTAAAGTCTGGCAGCCTCGAGACTGAAGATGACA	6529
	TGTCATCTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGGCATTGGCGTTTGCCT**A**AACCTGAAAGCCACCATTACCGAACTTCCCGGGTTTAGGGGAGATTCCCGGGGTTGGAAC	6530
	TTCAGGTT**T**AGGCAAAC	6531
	GTTTGCCT**A**AACCTGAA	6532

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Gln21Term CAA-TAA	ATGTTGAAGCTCTCGTGTAATGCGACTGATAAGTTACAGACCCTCT TCTCGCATTCTCATTAACCGGATCCGGCACACCGGAGAACCGTCT CCTCCGTGTCGTGCTCTCATCTGAGGAAAC	6533
	GTTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCTCCGGT GTGCCGGATCCGGTTAATGAGAATGCGAGAAGAGGGTCTGTAACT TATCAGTCGCATTACACGAGAGCTTCAACAT	6534
	ATTCTCATTAACCGGAT	6535
	ATCCGGTTAATGAGAAT	6536
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Arg28Term AGA-TGA	GCGACTGATAAGTTACAGACCCTCTTCTCGCATTCTCATCAACCGG ATCCGGCACACCGGTGAACCGTCTCCTCCGTGTCGTGCTCTCATC TGAGGAAACCGGTTCTCGATCCTTTGCGAG	6537
	CTCGCAAAGGATCGAGAACCGGTTTCCTCAGATGAGAGCACGACA CGGAGGAGACGGTTCACCGGTGTGCCGGATCCGGTTGATGAGAA TGCGAGAAGAGGGTCTGTAACTTATCAGTCGC	6538
	CACACCGGTGAACCGTC	6539
	GACGGTTCACCGGTGTG	6540
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Ser24Term TCG-TAG	CCCTCTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAA CCGTCTCCTCCGTGTAGTGCTCTCATCTGAGGAAACCGGTTCTCG ATCCTTTGCGAGCGATCGTATCTGCTGATCA	6541
	TGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTC CTCAGATGAGAGCACTACACGGAGGAGACGGTTCTCCGGTGTGC CGGATCCGGTTGATGAGAATGCGAGAAGAGGG	6542
	CTCCGTGTAGTGCTCTC	6543
	GAGAGCACTACACGGAG	6544
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Cys25Term TGC-TGA	CTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAACCGT CTCCTCCGTGTCGTGATCTCATCTGAGGAAACCGGTTCTCGATCC TTTGCGAGCGATCGTATCTGCTGATCAAGGA	6545
	TCCTTGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGG TTTCCTCAGATGAGATCACGACACGGAGGAGACGGTTCTCCGGTG TGCCGGATCCGGTTGATGAGAATGCGAGAAG	6546
	GTGTCGTGATCTCATCT	6547
	AGATGAGATCACGACAC	6548
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Leu2Term TTG-TAG	ATTCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGG GCATCAAAAATGTAGAAGCTTTCGTGTAATGTGACTAACAACTTAC ACACCTTCTCCTTCTTCTCCGATTCCTC	6549
	GAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCACA TTACACGAAAGCTTCTACATTTTTGATGCCCTTTTTTTTTTATGGTTC CTGAGGTTTTGGTTTATAGAAGAAGAAT	6550

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAATGT**A**GAAGCTTT	6551
	AAAGCTTC**T**ACATTTTT	6552
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Lys3Term AAG-TAG	TCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGGGCATCAAAAATGTTG**T**AGCTTTCGTGTAATGTGACTAACAACTTACACACCTTCTCCTTCTTCTCCGATTCCTCCC	6553
	GGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCACATTACACGAAAGCT**A**CAACATTTTTGATGCCCTTTTTTTTTTATGGTTCCTGAGGTTTTGGTTTATAGAAGAAGA	6554
	AAATGTTG**T**AGCTTTCG	6555
	CGAAAGCT**A**CAACATTT	6556
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Ser5Term TCG-TAG	CTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGGGCATCAAAAATGTTGAAGCTTT**A**GTGTAATGTGACTAACAACTTACACACCTTCTCCTTCTTCTCCGATTCCTCCCTTTTCAT	6557
	ATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCACATTACAC**T**AAAGCTTCAACATTTTTGATGCCCTTTTTTTTTTATGGTTCCTGAGGTTTTGGTTTATAG	6558
	GAAGCTTT**A**GTGTAATG	6559
	CATTACAC**T**AAAGCTTC	6560
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Cys6Term TGT-TGA	AAACCAAAACCTCAGGAACCATAAAAAAAAAAGGGCATCAAAAATGTTGAAGCTTTCGTG**A**AATGTGACTAACAACTTACACACCTTCTCCTTCTTCTCCGATTCCTCCCTTTTCATCCCG	6561
	CGGGATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCACATT**T**CACGAAAGCTTCAACATTTTTGATGCCCTTTTTTTTTTATGGTTCCTGAGGTTTTGGTTT	6562
	CTTTCGTG**A**AATGTGAC	6563
	GTCACATT**T**CACGAAAG	6564

Table 23
Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Lys4Term AAG-TAG	GGGAGAGCTCTAGCTCTGTAGAAAAGAAGGATTCATTCATCATATCCAGAAATGGCTCTA**T**AGTTTAACCCTTTGGTGGCATCTCAGCCTTACAAATTCCCTTCCTCGACTCGTCCGCCAA	6565
	TTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCTGAGATGCCACCAAAGGGTTAAACT**A**TAGAGCCATTTCTGGATATGATGAATGAATCCTTCTTTTCTACAGAGCTAGAGCTCTCCC	6566
	TGGCTCTA**T**AGTTTAAC	6567
	GTTAAACT**A**TAGAGCCA	6568
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Leu8Term TTG-TAG	CTCTGTAGAAAAGAAGGATTCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACCCTT**A**GGTGGCATCTCAGCCTTACAAATTCCCTTCCTCGACTCGTCCGCCAACTCCTTCTTTCAG	6569
	CTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCTGAGATGCCACC**T**AAGGGTTAAACTTTAGAGCCATTTCTGGATATGATGAATGAATCCTTCTTTTCTACAGAG	6570
	TAACCCTT**A**GGTGGCAT	6571
	ATGCCACC**T**AAGGGTTA	6572
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Gln12Term CAG-TAG	AGAAGGATTCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACCCTTTGGTGGCATCT**T**AGCCTTACAAATTCCCTTCCTCGACTCGTCCGCCAACTCCTTCTTTCAGATCTCCCAAGT	6573
	ACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCT**A**AGATGCCACCAAAGGGTTAAACTTTAGAGCCATTTCTGGATATGATGAATGAATCCTTCT	6574
	TGGCATCT**T**AGCCTTAC	6575
	GTAAGGCT**A**AGATGCCA	6576
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Phe14Term TAC-TAG	TCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACCCTTTGGTGGCATCTCAGCCTTA**G**AAATTCCCTTCCTCGACTCGTCCGCCAACTCCTTCTTTCAGATCTCCCAAGTTCCTCTGC	6577
	GCAGAGGAACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTT**C**TAAGGCTGAGATGCCACCAAAGGGTTAAACTTTAGAGCCATTTCTGGATATGATGAATGA	6578
	CAGCCTTA**G**AAATTCCC	6579
	GGGAATTT**C**TAAGGCTG	6580

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Brassica napus* Leu3Term TTG-TAG	GAGAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCAT**A**GAAGCTTAACCCTTTGGCATCTCAGCCTTACAAACTCCCTTCCTCGGCTCGTCCGCCAAT	6581
	ATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCTGAGATGCCAAAGGGTTAAGCTTC**T**ATGCCATTTTCTTTTTTTTGATACGAGGTTTGATGTTCTTTCAGACACGAGCGAGCTCTC	6582
	AATGGCAT**A**GAAGCTTA	6583
	TAAGCTTC**T**ATGCCATT	6584
Increased stearate stearoyl-ACP desaturase *Brassica napus* Lys4Term AAG-TAG	GAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATTG**T**AGCTTAACCCTTTGGCATCTCAGCCTTACAAACTCCCTTCCTCGGCTCGTCCGCCAATCT	6585
	AGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCTGAGATGCCAAAGGGTTAAGCT**A**CAATGCCATTTTCTTTTTTTTGATACGAGGTTTGATGTTCTTTCAGACACGAGCGAGCTC	6586
	TGGCATTG**T**AGCTTAAC	6587
	GTTAAGCT**A**CAATGCCA	6588
Increased stearate stearoyl-ACP desaturase *Brassica napus* Leu8Term TTG-TAG	TCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATTGAAGCTTAACCCTT**A**GGCATCTCAGCCTTACAAACTCCCTTCCTCGGCTCGTCCGCCAATCTCTACTCTCAGATC	6589
	GATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCTGAGATGCC**T**AAGGGTTAAGCTTCAATGCCATTTTCTTTTTTTTGATACGAGGTTTGATGTTCTTTCAGA	6590
	TAACCCTT**A**GGCATCTC	6591
	GAGATGCC**T**AAGGGTTA	6592
Increased stearate stearoyl-ACP desaturase *Brassica napus* Gln11Term CAG-TAG	AACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATTGAAGCTTAACCCTTTGGCATCT**T**AGCCTTACAAACTCCCTTCCTCGGCTCGTCCGCCAATCTCTACTCTCAGATCTCCCAAGT	6593
	ACTTGGGAGATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCT**A**AGATGCCAAAGGGTTAAGCTTCAATGCCATTTTCTTTTTTTTGATACGAGGTTTGATGTT	6594
	TGGCATCT**T**AGCCTTAC	6595
	GTAAGGCT**A**AGATGCCA	6596
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Gln27Term CAA-TAA	AACCAAAAGAAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTTTCCTTTCTT**T**AAACCCAAAAGTTACCTTCTTTCGCTCTTCCACCAATGGCCAGTACCAGATCTCCTAAGT	6597
	ACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAGGTAACTTTTGGGTTT**A**AGAAAGGAAAGGATTGAGCTTGAGAGCCATTGTTTTTTTTCTTACCTTTTTCTTTTGGTT	6598

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCTTTCT**T**AAACCCAA	6599
	TTGGGTTT**A**AGAAAGGA	6600
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Gln29Term CAA-TAA	AAGAAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTTTCCTTTCTCAAACC**T**AAAAGTTACCTTCTTTCGCTCTTCCACCAATGGCCAGTACCAGATCTCCTAAGTTCTACA	6601
	TGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAGGTAACTTTT**A**GGTTTGAGAAAGGAAAGGATTGAGCTTGAGAGCCATTGTTTTTTTTCTTACCTTTTTCTT	6602
	CTCAAACC**T**AAAAGTTA	6603
	TAACTTTT**A**GGTTTGAG	6604
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Lys30Term AAG-TAG	AAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTTTCCTTTCTCAAACCCAA**T**AGTTACCTTCTTTCGCTCTTCCACCAATGGCCAGTACCAGATCTCCTAAGTTCTACATGG	6605
	CCATGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAGGTAACT**A**TTGGGTTTGAGAAAGGAAAGGATTGAGCTTGAGAGCCATTGTTTTTTTTCTTACCTTTTT	6606
	AAACCCAA**T**AGTTACCT	6607
	AGGTAACT**A**TTGGGTTT	6608
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Lys46Term AAG-TAG	TCTCAAACCCAAAAGTTACCTTCTTTCGCTCTTCCACCAATGGCCAGTACCAGATCTCCT**T**AGTTCTACATGGCCTCTACCCTCAAGTCTGGTTCTAAGGAAGTTGAGAATCTCAAGAAGC	6609
	GCTTCTTGAGATTCTCAACTTCCTTAGAACCAGACTTGAGGGTAGAGGCCATGTAGAACT**A**AGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAGGTAACTTTTGGGTTTGAGA	6610
	GATCTCCT**T**AGTTCTAC	6611
	GTAGAACT**A**AGGAGATC	6612
Increased stearate stearoyl-ACP desaturase *Glycine max* Gln11Term CAA-TAA	TCTTCTGATTCATTTAATCTTTACTCATCAATGGCTCTGAGACTGAACCCTATCCCCACC**T**AAACCTTCTCCCTCCCCCAAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTA	6613
	TAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTTGGGGGAGGGAGAAGGTTT**A**GGTGGGGATAGGGTTCAGTCTCAGAGCCATTGATGAGTAAAGATTAAATGAATCAGAAGA	6614
	TCCCCACC**T**AAACCTTC	6615
	GAAGGTTT**A**GGTGGGGA	6616

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Glycine max* Gln17Term CAA-TAA	CTTTACTCATCAATGGCTCTGAGACTGAACCCTATCCCCACCCAAACCTTCTCCCTCCCC**T**AAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTACCCTCCGCTCCGGTTCCA	6617
	TGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTT**A**GGGGAGGGAGAAGGTTTGGGTGGGGATAGGGTTCAGTCTCAGAGCCATTGATGAGTAAAG	6618
	CCCTCCCC**T**AAATGGCC	6619
	GGCCATTT**A**GGGGAGGG	6620
Increased stearate stearoyl-ACP desaturase *Glycine max* Arg22Term AGA-TGA	GCTCTGAGACTGAACCCTATCCCCACCCAAACCTTCTCCCTCCCCCAAATGGCCAGTCTC**T**GATCTCCCAGGTTCCGCATGGCCTCTACCCTCCGCTCCGGTTCCAAAGAGGTTGAAAATA	6621
	TATTTTCAACCTCTTTGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGATC**A**GAGACTGGCCATTTGGGGGAGGGAGAAGGTTTGGGTGGGGATAGGGTTCAGTCTCAGAGC	6622
	CCAGTCTC**T**GATCTCCC	6623
	GGGAGATC**A**GAGACTGG	6624
Increased stearate stearoyl-ACP desaturase *Glycine max* Lys37Term AAA-TAA	CAAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTACCCTCCGCTCCGGTTCC**T**AAGAGGTTGAAAATATTAAGAAGCCATTCACTCCTCCCAGAGAAGTGCATGTTCAAGTAA	6625
	TTACTTGAACATGCACTTCTCTGGGAGGAGTGAATGGCTTCTTAATATTTTCAACCTCTT**A**GGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTTG	6626
	CCGGTTCC**T**AAGAGGTT	6627
	AACCTCTT**A**GGAACCGG	6628
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Gln11Term CAA-TAA	CAACAAGCACACACAAGAACAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTT**T**AATCAGACCTGTACCGTTCATTCGCGTTTCCTCAACCGAAACCTCTCAGATCTCCCAAAT	6629
	ATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATGAACGGTACAGGTCTGATT**A**AAACGTCGCCGTATTGATGCGAATCGCCATTGTTGATGTTGTTCTTGTGTGTGCTTGTTG	6630
	CGACGTTT**T**AATCAGAC	6631
	GTCTGATT**A**AAACGTCG	6632
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Ser12Term TCA-TGA	AAGCACACACAAGAACAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTTCAAT**G**AGACCTGTACCGTTCATTCGCGTTTCCTCAACCGAAACCTCTCAGATCTCCCAAATTCGC	6633
	GCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATGAACGGTACAGGTCT**C**ATTGAAACGTCGCCGTATTGATGCGAATCGCCATTGTTGATGTTGTTCTTGTGTGTGCTT	6634

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTTCAAT**G**AGACCTGT	6635
	ACAGGTCT**C**ATTGAAAC	6636
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Tyr15Term TAC-TAG	AAGAACAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTT CAATCAGACCTGTA**G**CGTTCATTCGCGTTTCCTCAACCGAAACCTC TCAGATCTCCCAAATTCGCCATGGCTTCC	6637
	GGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGG AAACGCGAATGAACG**C**TACAGGTCTGATTGAAACGTCGCCGTATT GATGCGAATCGCCATTGTTGATGTTGTTCTT	6638
	GACCTGTA**G**CGTTCATT	6639
	AATGAACG**C**TACAGGTC	6640
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Ser17Term TCA-TGA	CAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTTCAATC AGACCTGTACCGTT**G**ATTCGCGTTTCCTCAACCGAAACCTCTCAGA TCTCCCAAATTCGCCATGGCTTCCACCAT	6641
	ATGGTGGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGT TGAGGAAACGCGAAT**C**AACGGTACAGGTCTGATTGAAACGTCGCC GTATTGATGCGAATCGCCATTGTTGATGTTG	6642
	GTACCGTT**G**ATTCGCGT	6643
	ACGCGAAT**C**AACGGTAC	6644
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Arg4Term CGA-TGA	ACACACAACACACACTCAATCACACACACATCATCATCTTCTTCATC AACGATGGCGCTT**T**GAATGAGTCCGGTGACGCTTCAACGGGAGAT ATATCCTTCATACACTTTTCATCAATCGA	6645
	TCGATTGATGAAAAGTGTATGAAGGATATATCTCCCGTTGAAGCGT CACCGGACTCATTC**A**AAGCGCCATCGTTGATGAAGAAGATGATGA TGTGTGTGTGATTGAGTGTGTGTTGTGTGT	6646
	TGGCGCTT**T**GAATGAGT	6647
	ACTCATTC**A**AAGCGCCA	6648
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Gln11Term CAA-TAA	ACACACACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGA GTCCGGTGACGCTT**T**AACGGGAGATATATCCTTCATACACTTTTCA TCAATCGAAAAATCTCAGATCTCCTAAAT	6649
	ATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGG ATATATCTCCCGTT**A**AAGCGTCACCGGACTCATTCGAAGCGCCAT CGTTGATGAAGAAGATGATGATGTGTGTGT	6650
	TGACGCTT**T**AACGGGAG	6651
	CTCCCGTT**A**AAGCGTCA	6652

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Glu13Term GAG-TAG	ACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTGACGCTTCAACGG**T**AGATATATCCTTCATACACTTTTCATCAATCGAAAAATCTCAGATCTCCTAAATTCGCGA	6653
	TCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGGATATATCT**A**CCGTTGAAGCGTCACCGGACTCATTCGAAGCGCCATCGTTGATGAAGAAGATGATGATGT	6654
	TTCAACGG**T**AGATATAT	6655
	ATATATCT**A**CCGTTGAA	6656
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Tyr15Term TAT-TAG	ATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTGACGCTTCAACGGGAGATATA**G**CCTTCATACACTTTTCATCAATCGAAAAATCTCAGATCTCCTAAATTCGCGATGGCTTCC	6657
	GGAAGCCATCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGG**C**TATATCTCCCGTTGAAGCGTCACCGGACTCATTCGAAGCGCCATCGTTGATGAAGAAGAT	6658
	GAGATATA**G**CCTTCATA	6659
	TATGAAGG**C**TATATCTC	6660
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Lys4Term AAG-TAG	AACTCAGCCAGCTTGCCCCCAAACAACAGCGCAGAAAAACCTTCAACAACAATGGCTCTC**T**AGCTCAACCCAGTCACCACCTTCCCTTCAACACGCTCCCTCAACAACTTCTCCTCCAGAT	6661
	ATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTTGAAGGGAAGGTGGTGACTGGGTTGAGCT**A**GAGAGCCATTGTTGTTGAAGGTTTTTCTGCGCTGTTGTTTGGGGGCAAGCTGGCTGAGTT	6662
	TGGCTCTC**T**AGCTCAAC	6663
	GTTGAGCT**A**GAGAGCCA	6664
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Ser13Term TCA-TGA	GCGCAGAAAAACCTTCAACAACAATGGCTCTCAAGCTCAACCCAGTCACCACCTTCCCTT**G**AACACGCTCCCTCAACAACTTCTCCTCCAGATCTCCTCGCACCTTTCTCATGGCTGCTTC	6665
	GAAGCAGCCATGAGAAAGGTGCGAGGAGATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTT**C**AAGGGAAGGTGGTGACTGGGTTGAGCTTGAGAGCCATTGTTGTTGAAGGTTTTTCTGCGC	6666
	CTTCCCTT**G**AACACGCT	6667
	AGCGTGTT**C**AAGGGAAG	6668
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Arg23Term AGA-TGA	CTCAAGCTCAACCCAGTCACCACCTTCCCTTCAACACGCTCCCTCAACAACTTCTCCTCC**T**GATCTCCTCGCACCTTTCTCATGGCTGCTTCCACTTTCAATTCCACCTCCACCAAGTAAG	6669
	CTTACTTGGTGGAGGTGGAATTGAAAGTGGAAGCAGCCATGAGAAAGGTGCGAGGAGATC**A**GGAGGAGAAGTTGTTGAGGGAGCGTGTTGAAGGGAAGGTGGTGACTGGGTTGAGCTTGAG	6670

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCTCCTCC**T**GATCTCCT	6671
	AGGAGATC**A**GGAGGAGA	6672
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Lys41Term AAG-TAG	TCCTCCAGATCTCCTCGCACCTTTCTCATGGCTGCTTCCACTTTCAATTCCACCTCCACC**T**AGTAAGCATCTCCTCCTCCTCGGAATCTCCGCCGATTTCTTTTAAGCGATTGATCGTAGA	6673
	TCTACGATCAATCGCTTAAAAGAAATCGGCGGAGATTCCGAGGAGGAGGAGATGCTTACT**A**GGTGGAGGTGGAATTGAAAGTGGAAGCAGCCATGAGAAAGGTGCGAGGAGATCTGGAGGA	6674
	CCTCCACC**T**AGTAAGCA	6675
	TGCTTACT**A**GGTGGAGG	6676
Increased stearate stearoyl-ACP desaturase *Olea europaea* Arg21Term AGA-TGA	ATGGCACTGAAACTTTGCTTTCCACCCCACAAGATGCCTTCCTTCCCCGATGCTCGTATC**T**GATCTCACAGGGTTTTCATGGCTTCAACTATTCATTCTCCTTCTATGGAGGTCGGAAAAG	6677
	CTTTTCCGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAAAACCCTGTGAGATC**A**GATACGAGCATCGGGGAAGGAAGGCATCTTGTGGGGTGGAAAGCAAAGTTTCAGTGCCAT	6678
	CTCGTATC**T**GATCTCAC	6679
	GTGAGATC**A**GATACGAG	6680
Increased stearate stearoyl-ACP desaturase *Olea europaea* Ser29Term TCA-TGA	CCCACAAGATGCCTTCCTTCCCCGATGCTCGTATCAGATCTCACAGGGTTTTCATGGCTT**G**AACTATTCATTCTCCTTCTATGGAGGTCGGAAAAGTTAAAAAGCCTTTCACGCCTCCACG	6681
	CGTGGAGGCGTGAAAGGCTTTTTAACTTTTCCGACCTCCATAGAAGGAGAATGAATAGTT**C**AAGCCATGAAAACCCTGTGAGATCTGATACGAGCATCGGGGAAGGAAGGCATCTTGTGGG	6682
	CATGGCTT**G**AACTATTC	6683
	GAATAGTT**C**AAGCCATG	6684
Increased stearate stearoyl-ACP desaturase *Olea europaea* Glu37Term GAG-TAG	GATGCTCGTATCAGATCTCACAGGGTTTTCATGGCTTCAACTATTCATTCTCCTTCTATG**T**AGGTCGGAAAAGTTAAAAAGCCTTTCACGCCTCCACGAGAGGTACATGTTCAAGTAACCC	6685
	GGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAGGCTTTTTAACTTTTCCGACCT**A**CATAGAAGGAGAATGAATAGTTGAAGCCATGAAAACCCTGTGAGATCTGATACGAGCATC	6686
	CTTCTATG**T**AGGTCGGA	6687
	TCCGACCT**A**CATAGAAG	6688

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Olea europaea* Gly39Term GGA-TGA	CGTATCAGATCTCACAGGGTTTTCATGGCTTCAACTATTCATTCTCCTTCTATGGAGGTC**T**GAAAAGTTAAAAAGCCTTTCACGCCTCCACGAGAGGTACATGTTCAAGTAACCCATTCCT	6689
	AGGAATGGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAGGCTTTTTAACTTTTC**A**GACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAAAACCCTGTGAGATCTGATACG	6690
	TGGAGGTC**T**GAAAAGTT	6691
	AACTTTTC**A**GACCTCCA	6692
Increased stearate stearoyl-ACP desaturase *Persea americana* Lys4Term AAA-TAA	TTCTCGTTTTTGTCGTCCCCTCTGCTCTCTCTCTCTATCAGGCACGGAGAAATGGCACTG**T**AACTCAGTCCAGTCATGTTTCAATCTCAGAAGCTTCCATTTCTTGCCTCCTATCCGCCTT	6693
	AAGGCGGATAGGAGGCAAGAAATGGAAGCTTCTGAGATTGAAACATGACTGGACTGAGTT**A**CAGTGCCATTTCTCCGTGCCTGATAGAGAGAGAGAGCAGAGGGGACGACAAAAACGAGAA	6694
	TGGCACTG**T**AACTCAGT	6695
	ACTGAGTT**A**CAGTGCCA	6696
Increased stearate stearoyl-ACP desaturase *Persea americana* Gln11Term CAA-TAA	CTGCTCTCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTCATGTTT**T**AATCTCAGAAGCTTCCATTTCTTGCCTCCTATCCGCCTTCCAATCTCAGATCTCCGAGGG	6697
	CCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAATGGAAGCTTCTGAGATT**A**AAACATGACTGGACTGAGTTTCAGTGCCATTTCTCCGTGCCTGATAGAGAGAGAGAGCAG	6698
	TCATGTTT**T**AATCTCAG	6699
	CTGAGATT**A**AAACATGA	6700
Increased stearate stearoyl-ACP desaturase *Persea americana* Gln13Term CAG-TAG	TCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTCATGTTTCAATCT**T**AGAAGCTTCCATTTCTTGCCTCCTATCCGCCTTCCAATCTCAGATCTCCGAGGGTTTTCA	6701
	TGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAATGGAAGCTTCT**A**AGATTGAAACATGACTGGACTGAGTTTCAGTGCCATTTCTCCGTGCCTGATAGAGAGAGA	6702
	TTCAATCT**T**AGAAGCTT	6703
	AAGCTTCT**A**AGATTGAA	6704
Increased stearate stearoyl-ACP desaturase *Persea americana* Lys14Term AAG-TAG	CTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTCATGTTTCAATCTCAG**T**AGCTTCCATTTCTTGCCTCCTATCCGCCTTCCAATCTCAGATCTCCGAGGGTTTTCATGG	6705
	CCATGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAATGGAAGCT**A**CTGAGATTGAAACATGACTGGACTGAGTTTCAGTGCCATTTCTCCGTGCCTGATAGAGAG	6706

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCTCAG**T**AGCTTCCA	6707
	TGGAAGCT**A**CTGAGATT	6708
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Tyr12Term TAC-TAG	CCCCGAGATCTCGCTGCCGCTGCTCATGGCGTTCGCGGCGTCCC ACACCGCATCGCCGTA**G**TCCTGCGGCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCGAAGATGGTGGCCATGGCC	6709
	GGCCATGGCCACCATCTTCGACATCCCATTGCTCCTCCTCTGCGC CACGCCGCCGCAGGA**C**TACGGCGATGCGGTGTGGGACGCCGCG AACGCCATGAGCAGCGGCAGCGAGATCTCGGGG	6710
	TCGCCGTA**G**TCCTGCGG	6711
	CCGCAGGA**C**TACGGCGA	6712
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Gln19Term CAG-TAG	CTGCTCATGGCGTTCGCGGCGTCCCACACCGCATCGCCGTACTC CTGCGGCGGCGTGGCG**T**AGAGGAGGAGCAATGGGATGTCGAAGA TGGTGGCCATGGCCTCCACCATCAACAGGGTCA	6713
	TGACCCTGTTGATGGTGGAGGCCATGGCCACCATCTTCGACATCC CATTGCTCCTCCTCT**A**CGCCACGCCGCCGCAGGAGTACGGCGAT GCGGTGTGGGACGCCGCGAACGCCATGAGCAG	6714
	GCGTGGCG**T**AGAGGAGG	6715
	CCTCCTCT**A**CGCCACGC	6716
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Ser26Term TCG-TAG	CCCACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCGCAGAG GAGGAGCAATGGGATGT**A**GAAGATGGTGGCCATGGCCTCCACCA TCAACAGGGTCAAGACTGCTAAGAAGCCCTACAC	6717
	GTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGGCC ATGGCCACCATCTTC**T**ACATCCCATTGCTCCTCCTCTGCGCCACG CCGCCGCAGGAGTACGGCGATGCGGTGTGGG	6718
	TGGGATGT**A**GAAGATGG	6719
	CCATCTTC**T**ACATCCCA	6720
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Lys27Term AAG-TAG	CACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCG**T**AGATGGTGGCCATGGCCTCCACCATCAA CAGGGTCAAGACTGCTAAGAAGCCCTACACTC	6721
	GAGTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGG CCATGGCCACCATCT**A**CGACATCCCATTGCTCCTCCTCTGCGCCA CGCCGCCGCAGGAGTACGGCGATGCGGTGTG	6722
	GGATGTCG**T**AGATGGTG	6723
	CACCATCT**A**CGACATCC	6724

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Leu3Term TTG-TAG	TTCTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGAGAGAAGCAATGGCGT**A**GAAGCTTCACCACACGGCCTTCAATCCTTCCATGGCGGTTACCTCTTCGGGACTTCCTCG	6725
	CGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAGGCCGTGTGGTGAAGCTTC**T**ACGCCATTGCTTCTCTCTCCTAAGTGCTTCTGTTGGTAACCGCTCAACCTAGAGAGAGAA	6726
	AATGGCGT**A**GAAGCTTC	6727
	GAAGCTTC**T**ACGCCATT	6728
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Lys4Term AAG-TAG	CTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGAGAGAAGCAATGGCGTTG**T**AGCTTCACCACACGGCCTTCAATCCTTCCATGGCGGTTACCTCTTCGGGACTTCCTCGAT	6729
	ATCGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAGGCCGTGTGGTGAAGCT**A**CAACGCCATTGCTTCTCTCTCCTAAGTGCTTCTGTTGGTAACCGCTCAACCTAGAGAGAG	6730
	TGGCGTTG**T**AGCTTCAC	6731
	GTGAAGCT**A**CAACGCCA	6732
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Ser19Term TCG-TAG	AAGCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCATGGCGGTTACCTCTT**A**GGGACTTCCTCGATCGTATCACCTCAGATCTCACCGCGTTTTCATGGCTTCTTCTACAAT	6733
	ATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGATACGATCGAGGAAGTCCC**T**AAGAGGTAACCGCCATGGAAGGATTGAAGGCCGTGTGGTGAAGCTTCAACGCCATTGCTT	6734
	TACCTCTT**A**GGGACTTC	6735
	GAAGTCCC**T**AAGAGGTA	6736
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Gly20Term GGA-TGA	GCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCATGGCGGTTACCTCTTCG**T**GACTTCCTCGATCGTATCACCTCAGATCTCACCGCGTTTTCATGGCTTCTTCTACAATTG	6737
	CAATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGATACGATCGAGGAAGTC**A**CGAAGAGGTAACCGCCATGGAAGGATTGAAGGCCGTGTGGTGAAGCTTCAACGCCATTGC	6738
	CCTCTTCG**T**GACTTCCT	6739
	AGGAAGTC**A**CGAAGAGG	6740
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Ser21Term TCA-TGA	TGGCTCTGAATCTCAACCCCGTTTCCACACCATTTCAGTGTCGTCGATTGCCGTCTTTCT**G**ACCTCGTCAAACGCCTTCTCGCAGATCTCCCAAATTCTTCATGGCTTCCACTCTCAGCAG	6741
	CTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATCTGCGAGAAGGCGTTTGACGAGGT**C**AGAAAGACGGCAATCGACGACACTGAAATGGTGTGGAAACGGGGTTGAGATTCAGAGCCA	6742

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTCTTTCT**G**ACCTCGTC	6743
	GACGAGGT**C**AGAAAGAC	6744
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Gln24Term CAA-TAA	AATCTCAACCCCGTTTCCACACCATTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGT**T**AAACGCCTTCTCGCAGATCTCCCAAATTCTTCATGGCTTCCACTCTCAGCAGCTCTTCTC	6745
	GAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATCTGCGAGAAGGCGTTT**A**ACGAGGTGAGAAAGACGGCAATCGACGACACTGAAATGGTGTGGAAACGGGGTTGAGATT	6746
	CACCTCGT**T**AAACGCCT	6747
	AGGCGTTT**A**ACGAGGTG	6748
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Arg29Term AGA-TGA	TCCACACCATTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTCAAACGCCTTCTCGC**T**GATCTCCCAAATTCTTCATGGCTTCCACTCTCAGCAGCTCTTCTCCTAAGGAAGCGGAAA	6749
	TTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATC**A**GCGAGAAGGCGTTTGACGAGGTGAGAAAGACGGCAATCGACGACACTGAAATGGTGTGGA	6750
	CTTCTCGC**T**GATCTCCC	6751
	GGGAGATC**A**GCGAGAAG	6752
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Lys32Term AAA-TAA	TTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTCAAACGCCTTCTCGCAGATCTCCC**T**AATTCTTCATGGCTTCCACTCTCAGCAGCTCTTCTCCTAAGGAAGCGGAAAGCCTGAAGA	6753
	TCTTCAGGCTTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATT**A**GGGAGATCTGCGAGAAGGCGTTTGACGAGGTGAGAAAGACGGCAATCGACGACACTGAAA	6754
	GATCTCCC**T**AATTCTTC	6755
	GAAGAATT**A**GGGAGATC	6756
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Leu10Term TTA-TGA	AAATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCGT**G**AAAATCTCACAAAATGTTACCATTTCCTTGTTCTTCAGCCAGATCTGAGCGAGTTTTCAT	6757
	ATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAACATTTTGTGAGATTTT**C**ACGACACCCCATTGATATTCAGTGCCATTGTTGATGCTCTGTTTTTCACCTCGACTATTT	6758
	GGTGTCGT**G**AAAATCTC	6759
	GAGATTTT**C**ACGACACC	6760

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Lys11Term AAA-TAA	ATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCGTTA**T**AATCTCACAAAATGTTACCATTTCCTTGTTCTTCAGCCAGATCTGAGCGAGTTTTCATGG	6761
	CCATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAACATTTTGTGAGATT**A**TAACGACACCCCATTGATATTCAGTGCCATTGTTGATGCTCTGTTTTTCACCTCGACTAT	6762
	TGTCGTTA**T**AATCTCAC	6763
	GTGAGATT**A**TAACGACA	6764
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Lys14Term AAA-TAA	GTGAAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCGTTAAAATCTCAC**T**AAATGTTACCATTTCCTTGTTCTTCAGCCAGATCTGAGCGAGTTTTCATGGCTTCAACCA	6765
	TGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAACATTT**A**GTGAGATTTTAACGACACCCCATTGATATTCAGTGCCATTGTTGATGCTCTGTTTTTCAC	6766
	AATCTCAC**T**AAATGTTA	6767
	TAACATTT**A**GTGAGATT	6768
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Leu16Term TTA-TGA	ACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCGTTAAAATCTCACAAAATGT**G**ACCATTTCCTTGTTCTTCAGCCAGATCTGAGCGAGTTTTCATGGCTTCAACCATTCATCG	6769
	CGATGAATGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGT**C**ACATTTTGTGAGATTTTAACGACACCCCATTGATATTCAGTGCCATTGTTGATGCTCTGT	6770
	CAAAATGT**G**ACCATTTC	6771
	GAAATGGT**C**ACATTTTG	6772
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser21Term TCA-TGA	TGGCTCTGAGGCTGAACCCTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCAT**G**ATCTTCTTCTTCTTCATCGTTCTCGCTTCCTCAAATGGCTAGCCTCAGATCTCCAAGGTT	6773
	AACCTTGGAGATCTGAGGCTAGCCATTTGAGGAAGCGAGAACGATGAAGAAGAAGAAGAT**C**ATGATGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAGGGTTCAGCCTCAGAGCCA	6774
	TTCATCAT**G**ATCTTCTT	6775
	AAGAAGAT**C**ATGATGAA	6776
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser26Term TCA-TGA	ACCCTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCTTCTTCTTCTT**G**ATCGTTCTCGCTTCCTCAAATGGCTAGCCTCAGATCTCCAAGGTTCCGCATGGCCTCCAC	6777
	GTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCATTTGAGGAAGCGAGAACGAT**C**AAGAAGAAGAAGATGATGATGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAGGGT	6778

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTCTTCTT**G**ATCGTTCT	6779
	AGAACGAT**C**AAGAAGAA	6780
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser27Term TCG-TAG	CTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCTTCTTCTTCTTCAT**A**GTTCTCGCTTCCTCAAATGGCTAGCCTCAGATCTCCAAGGTTCCGCATGGCCTCCACCCT	6781
	AGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCATTTGAGGAAGCGAGAAC**T**ATGAAGAAGAAGAAGATGATGATGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAG	6782
	TTCTTCAT**A**GTTCTCGC	6783
	GCGAGAAC**T**ATGAAGAA	6784
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser29Term TCG-TAG	CTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCTTCTTCTTCTTCATCGTTCT**A**GCTTCCTCAAATGGCTAGCCTCAGATCTCCAAGGTTCCGCATGGCCTCCACCCTCCGCAC	6785
	GTGCGGAGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCATTTGAGGAAGC**T**AGAACGATGAAGAAGAAGAAGATGATGATGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAG	6786
	ATCGTTCT**A**GCTTCCTC	6787
	GAGGAAGC**T**AGAACGAT	6788
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Leu3Term TTG-TAG	AAAGTTAAAAGCCGTCCAAAACCCAAACCAGGAAAGGCAAACGAAAAGAAAAAAATGGCTT**A**GAATTTTAATGCCATCGCCTCGAAATCTCAGAAGCTCCCTTGCTTTGCTCTTCCACCAAA	6789
	TTTGGTGGAAGAGCAAAGCAAGGGAGCTTCTGAGATTTCGAGGCGATGGCATTAAAATTC**T**AAGCCATTTTTTTCTTTTCGTTTGCCTTTCCTGGTTTGGGTTTTGGACGGCTTTTAACTTT	6790
	AATGGCTT**A**GAATTTTA	6791
	TAAAATTC**T**AAGCCATT	6792
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Ser1-Term TCG-TAG	CCCAAACCAGGAAAGGCAAACGAAAAGAAAAAAATGGCTTTGAATTTTAATGCCATCGCCT**A**GAAATCTCAGAAGCTCCCTTGCTTTGCTCTTCCACCAAAGGCCACCCTTAGATCTCCCAA	6793
	TTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAAAGCAAGGGAGCTTCTGAGATTTC**T**AGGCGATGGCATTAAAATTCAAAGCCATTTTTTCTTTTCGTTTGCCTTTCCTGGTTTGGG	6794
	CATCGCCT**A**GAAATCTC	6795
	GAGATTTC**T**AGGCGATG	6796

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Lys11Term AAA-TAA	CAAACCAGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTTTAATGCCATCGCCTCG**T**AATCTCAGAAGCTCCCTTGCTTTGCTCTTCCACCAAAGGCCACCCTTAGATCTCCCAAGT	6797
	ACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAAAGCAAGGGAGCTTCTGAGATT**A**CGAGGCGATGGCATTAAAATTCAAAGCCATTTTTTCTTTTCGTTTGCCTTTCCTGGTTTG	6798
	TCGCCTCG**T**AATCTCAG	6799
	CTGAGATT**A**CGAGGCGA	6800
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Gln13Term CAG-TAG	AGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTTTAATGCCATCGCCTCGAAATCT**T**AGAAGCTCCCTTGCTTTGCTCTTCCACCAAAGGCCACCCTTAGATCTCCCAAGTTTTCCA	6801
	TGGAAAACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAAAGCAAGGGAGCTTCT**A**AGATTTCGAGGCGATGGCATTAAAATTCAAAGCCATTTTTTCTTTTCGTTTGCCTTTCCT	6802
	CGAAATCT**T**AGAAGCTC	6803
	GAGCTTCT**A**AGATTTCG	6804

Table 24
Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Ser4Term TCG-TAG	AATAGAACGACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGC TCCAATGGCGAGCT**A**GGTTTTATCAGAATGTGGTTTTAGACCTCTC CCCAGATTCTACCCTAAACACACAACCTC	6805
	GAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTAAAACCA CATTCTGATAAAACC**T**AGCTCGCCATTGGAGCCTCTTCCCAAGAAG AAAAGAGGAAAAAGTCTCTGTCGTTCTATT	6806
	GGCGAGCT**T**GGTTTTAT	6807
	ATAAAACC**A**AGCTCGCC	6808
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Leu6Term TTA-TGA	ACGACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAAT GGCGAGCTCGGTTT**G**ATCAGAATGTGGTTTTAGACCTCTCCCCAG ATTCTACCCTAAACACACAACCTCTTTTGC	6809
	GCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTA AAACCACATTCTGAT**C**AAACCGAGCTCGCCATTGGAGCCTCTTCC CAAGAAGAAAAGAGGAAAAAGTCTCTGTCGT	6810
	CTCGGTTT**G**ATCAGAAT	6811
	ATTCTGAT**C**AAACCGAG	6812
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Ser7Term TCA-TGA	ACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAATGGC GAGCTCGGTTTTAT**G**AGAATGTGGTTTTAGACCTCTCCCCAGATTC TACCCTAAACACACAACCTCTTTTGCCTC	6813
	GAGGCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGT CTAAAACCACATTCT**C**ATAAAACCGAGCTCGCCATTGGAGCCTCTT CCCAAGAAGAAAAGAGGAAAAAGTCTCTGT	6814
	GGTTTTAT**G**AGAATGTG	6815
	CACATTCT**C**ATAAAACC	6816
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Glu8Term GAA-TAA	AGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAATGGCGA GCTCGGTTTTATCA**T**AATGTGGTTTTAGACCTCTCCCCAGATTCTA CCCTAAACACACAACCTCTTTTGCCTCTA	6817
	TAGAGGCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAG GTCTAAAACCACATT**A**TGATAAAACCGAGCTCGCCATTGGAGCCTC TTCCCAAGAAGAAAAGAGGAAAAAGTCTCT	6818
	TTTTATCA**T**AATGTGGT	6819
	ACCACATT**A**TGATAAAA	6820

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Leu4Term TTG-TAG	TCATCATCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACT**A**GGTCTTATCCGAATGTGGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCAC	6821
	GTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCACATTCGGATAAGACC**T**AGTTCGCCATTGCTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAGAAGAAGAAGATGATGA	6822
	GGCGAACT**A**GGTCTTAT	6823
	ATAAGACC**T**AGTTCGCC	6824
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Leu6Term TTA-TGA	TCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACTTGGTCT**G**ATCCGAATGTGGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCACTTTCCT	6825
	AGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCACATTCGGAT**C**AGACCAAGTTCGCCATTGCTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAGAAGAAGAAGA	6826
	CTTGGTCT**G**ATCCGAAT	6827
	ATTCGGAT**C**AGACCAAG	6828
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Glu8Term GAA-TAA	TTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACTTGGTCTTATCC**T**AATGTGGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCACTTTCCTCTCCA	6829
	TGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCACATT**A**GGATAAGACCAAGTTCGCCATTGCTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAGAAGAA	6830
	TCTTATCC**T**AATGTGGC	6831
	GCCACATT**A**GGATAAGA	6832
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Cys9Term TGT-TGA	CTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACTTGGTCTTATCCGAATG**A**GGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCACTTTCCTCTCCAACACC	6833
	GGTGTTGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCC**T**CATTCGGATAAGACCAAGTTCGCCATTGCTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAG	6834
	TCCGAATG**A**GGCATAAG	6835
	CTTATGCC**T**CATTCGGA	6836
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Trp5Term TGG-TGA	ATAACAGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTGGTTG**A**GTATTATCAGAATGTGGTTTAAGGCCTCTCCCAAGAATCTACTCACGACCCAGAATTGGT	6837
	ACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACCACATTCTGATAATAC**T**CAACCAGCAGCCATTGAAAACCCAGAAGCTAAAAATGCAAGAATTCAGCAATTCTGTTAT	6838

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCTGGTTG**A**GTATTATC	6839
	GATAATAC**T**CAACCAGC	6840
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Leu7Term TTA-TGA	AGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTGGTTGGGTAT**G**ATCAGAATGTGGTTTAAGGCCTCTCCCAAGAATCTACTCACGACCCAGAATTGGTTTTAC	6841
	GTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACCACATTCTGAT**C**ATACCCAACCAGCAGCCATTGAAAACCCAGAAGCTAAAAATGCAAGAATTCAGCAATTCT	6842
	TTGGGTAT**G**ATCAGAAT	6843
	ATTCTGAT**C**ATACCCAA	6844
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Ser8Term TCA-TGA	ATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTGGTTGGGTATTAT**G**AGAATGTGGTTTAAGGCCTCTCCCAAGAATCTACTCACGACCCAGAATTGGTTTTACATC	6845
	GATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACCACATTCT**C**ATAATACCCAACCAGCAGCCATTGAAAACCCAGAAGCTAAAAATGCAAGAATTCAGCAAT	6846
	GGTATTAT**G**AGAATGTG	6847
	CACATTCT**C**ATAATACC	6848
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Glu9Term GAA-TAA	TGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTGGTTGGGTATTATCA**T**AATGTGGTTTAAGGCCTCTCCCAAGAATCTACTCACGACCCAGAATTGGTTTTACATCGA	6849
	TCGATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACCACATT**A**TGATAATACCCAACCAGCAGCCATTGAAAACCCAGAAGCTAAAAATGCAAGAATTCAGCA	6850
	TATTATCA**T**AATGTGGT	6851
	ACCACATT**A**TGATAATA	6852
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Arg22Term AGA-TGA	GCAAGTTGGGTTTTATCAGAATGTGGTCTTAGACCACTCCCAAGAATCTACCCTAAGCCC**T**GAACTGGGGCAGCCACTTCTGCCTCCTCTCACATTAAGTTGAGAATTTCACGTACAGATC	6853
	GATCTGTACGTGAAATTCTCAACTTAATGTGAGAGGAGGCAGAAGTGGCTGCCCCAGTTC**A**GGGCTTAGGGTAGATTCTTGGGAGTGGTCTAAGACCACATTCTGATAAAACCCAACTTGC	6854
	CTAAGCCC**T**GAACTGGG	6855
	CCCAGTTC**A**GGGCTTAG	6856

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Lys34Term AAG-TAG	CTCCCAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCCTCTCACATT**T**AGTTGAGAATTTCACGTACAGATCTGAGTGGTTCTGCAATTTCTTTGTCTAATACTAATA	6857
	TATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACGTGAAATTCTCAACT**A**AATGTGAGAGGAGGCAGAAGTGGCTGCCCCAGTTCTGGGCTTAGGGTAGATTCTTGGGAG	6858
	CTCACATT**T**AGTTGAGA	6859
	TCTCAACT**A**AATGTGAG	6860
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Leu35Term TTG-TAG	CAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCCTCTCACATTAAGT**A**GAGAATTTCACGTACAGATCTGAGTGGTTCTGCAATTTCTTTGTCTAATACTAATAAAGA	6861
	TCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACGTGAAATTCTC**T**ACTTAATGTGAGAGGAGGCAGAAGTGGCTGCCCCAGTTCTGGGCTTAGGGTAGATTCTTG	6862
	CATTAAGT**A**GAGAATTT	6863
	AAATTCTC**T**ACTTAATG	6864
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Arg36Term AGA-TGA	AGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCCTCTCACATTAAGTTG**T**GAATTTCACGTACAGATCTGAGTGGTTCTGCAATTTCTTTGTCTAATACTAATAAAGAGA	6865
	TCTCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACGTGAAATTC**A**CAACTTAATGTGAGAGGAGGCAGAAGTGGCTGCCCCAGTTCTGGGCTTAGGGTAGATTCT	6866
	TTAAGTTG**T**GAATTTCA	6867
	TGAAATTC**A**CAACTTAA	6868
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Arg22Term AGA-TGA	GCGAGTTGGGTTTTATCAGAATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCA**T**GAACTGGCCACCCTTTGTTGAATTCCAATCCCACAAAGCTGAGATTTTCAAGAACAGATC	6869
	GATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTCAACAAAGGGTGGCCAGTTC**A**TGGCTTAGGATAGACCCTCGGGAGTGGCCTCAGACCACATTCTGATAAAACCCAACTCGC	6870
	CTAAGCCA**T**GAACTGGC	6871
	GCCAGTTC**A**TGGCTTAG	6872
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Leu27Term TTG-TAG	CAGAATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTT**A**GTTGAATTCCAATCCCACAAAGCTGAGATTTTCAAGAACAGATCTTGGAAATGGTTCTTC	6873
	GAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTCAAC**T**AAGGGTGGCCAGTTCTTGGCTTAGGATAGACCCTCGGGAGTGGCCTCAGACCACATTCTG	6874

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCACCCTT**A**GTTGAATT	6875
	AATTCAAC**T**AAGGGTGG	6876
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Leu28Term TTG-TAG	AATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGT**A**GAATTCCAATCCCACAAAGCTGAGATTTTCAAGAACAGATCTTGGAAATGGTTCTTCATT	6877
	AATGAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTC**T**ACAAAGGGTGGCCAGTTCTTGGCTTAGGATAGACCCTCGGGAGTGGCCTCAGACCACATT	6878
	CCCTTTGT**A**GAATTCCA	6879
	TGGAATTC**T**ACAAAGGG	6880
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Lys34Term AAG-TAG	CTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGTTGAATTCCAATCCCACA**T**AGCTGAGATTTTCAAGAACAGATCTTGGAAATGGTTCTTCATTCTGTTTGTCGAGTGGGA	6881
	TCCCACTCGACAAACAGAATGAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCT**A**TGTGGGATTGGAATTCAACAAAGGGTGGCCAGTTCTTGGCTTAGGATAGACCCTCGGGAG	6882
	ATCCCACA**T**AGCTGAGA	6883
	TCTCAGCT**A**TGTGGGAT	6884
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Tyr3Term TAC-TAG	CATCAGAGCGGCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCTATGAGTTA**G**GTCGTCAGAGAGCTAGCCATCGTGTTCGCACTAGCTGCTGGAGCTGCTTACCTCAACAAT	6885
	ATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGCTAGCTCTCTGACGAC**C**TAACTCATAGACTTCCATGGATTCTTAACCCAGCAATGCTTAGGTATCGCCGCTCTGATG	6886
	ATGAGTTA**G**GTCGTCAG	6887
	CTGACGAC**C**TAACTCAT	6888
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Arg6Term AGA-TGA	GCGGCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCTATGAGTTACGTCGTC**T**GAGAGCTAGCCATCGTGTTCGCACTAGCTGCTGGAGCTGCTTACCTCAACAATTGGCTTG	6889
	CAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGCTAGCTCTC**A**GACGACGTAACTCATAGACTTCCATGGATTCTTAACCCAGCAATGCTTAGGTATCGCCGC	6890
	ACGTCGTC**T**GAGAGCTA	6891
	TAGCTCTC**A**GACGACGT	6892

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Glu7Term GAG-TAG	GCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCTATGAGTTACGTCGTCAGA**T**AGCTAGCCATCGTGTTCGCACTAGCTGCTGGAGCTGCTTACCTCAACAATTGGCTTGTTT	6893
	AAACAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGCTAGCT**A**TCTGACGACGTAACTCATAGACTTCCATGGATTCTTAACCCAGCAATGCTTAGGTATCGC	6894
	TCGTCAGA**T**AGCTAGCC	6895
	GGCTAGCT**A**TCTGACGA	6896
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Gly17Term GGA-TGA	CCATGGAAGTCTATGAGTTACGTCGTCAGAGAGCTAGCCATCGTGTTCGCACTAGCTGCT**T**GAGCTGCTTACCTCAACAATTGGCTTGTTTGGCCTCTCTATTGGATTGCTCAAGGAACCA	6897
	TGGTTCCTTGAGCAATCCAATAGAGAGGCCAAACAAGCCAATTGTTGAGGTAAGCAGCTC**A**AGCAGCTAGTGCGAACACGATGGCTAGCTCTCTGACGACGTAACTCATAGACTTCCATGG	6898
	TAGCTGCT**T**GAGCTGCT	6899
	AGCAGCTC**A**AGCAGCTA	6900
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Arg22Term AGA-TGA	GCAAGTTGGGTTCTATCAGAATGTGGTCTTAGACCACTACCAAGAATATACCCAAAGCCC**T**GAATAGGGTCTTCTTCCGTTTGCGCCACCAATTTAAATCTGAGAAGAATTTCACCTTCAC	6901
	GTGAAGGTGAAATTCTTCTCAGATTTAAATTGGTGGCGCAAACGGAAGAAGACCCTATTC**A**GGGCTTTGGGTATATTCTTGGTAGTGGTCTAAGACCACATTCTGATAGAACCCAACTTGC	6902
	CAAAGCCC**T**GAATAGGG	6903
	CCCTATTC**A**GGGCTTTG	6904
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Cys29Term TGC-TGA	TGGTCTTAGACCACTACCAAGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTG**A**GCCACCAATTTAAATCTGAGAAGAATTTCACCTTCACCTATACGAACAGATCGGAATTGT	6905
	ACAATTCCGATCTGTTCGTATAGGTGAAGGTGAAATTCTTCTCAGATTTAAATTGGTGGC**T**CAAACGGAAGAAGACCCTATTCTGGGCTTTGGGTATATTCTTGGTAGTGGTCTAAGACCA	6906
	TCCGTTTG**A**GCCACCAA	6907
	TTGGTGGC**T**CAAACGGA	6908
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Leu33Term TTA-TGA	CACTACCAAGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTGCGCCACCAATT**G**AAATCTGAGAAGAATTTCACCTTCACCTATACGAACAGATCGGAATTGTTGGGCATTGAG	6909
	CTCAATGCCCAACAATTCCGATCTGTTCGTATAGGTGAAGGTGAAATTCTTCTCAGATTT**C**AATTGGTGGCGCAAACGGAAGAAGACCCTATTCTGGGCTTTGGGTATATTCTTGGTAGTG	6910

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CACCAATT**G**AAATCTGA	6911
	TCAGATTT**C**AATTGGTG	6912
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Arg36Term AGA-TGA	AGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTGCGCCACCAATTTAAATCTG**T**GAAGAATTTCACCTTCACCTATACGAACAGATCGGAATTGTTGGGCATTGAGGGTAAGTG	6913
	CACTTACCCTCAATGCCCAACAATTCCGATCTGTTCGTATAGGTGAAGGTGAAATTCTTC**A**CAGATTTAAATTGGTGGCGCAAACGGAAGAAGACCCTATTCTGGGCTTTGGGTATATTCT	6914
	TAAATCTG**T**GAAGAATT	6915
	AATTCTTC**A**CAGATTTA	6916
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Trp4Term TGG-TGA	CTCTTTATTATCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAGTTG**A**GTGATTTCAGAATGTGGGCTAAGGCCACTTCCAAGAATCTATGCCAGGCCCAGAAGTGGA	6917
	TCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGCCTTAGCCCACATTCTGAAATCAC**T**CAACTTGCCATAGGTGACTCAGAACTCAAAAAAAACAAAGAAGAGGAGGATAATAAAGAG	6918
	GCAAGTTG**A**GTGATTTC	6919
	GAAATCAC**T**CAACTTGC	6920
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Ser7Term TCA-TGA	TATCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAGTTGGGTGATTT**G**AGAATGTGGGCTAAGGCCACTTCCAAGAATCTATGCCAGGCCCAGAAGTGGAGCTTCATG	6921
	CATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGCCTTAGCCCACATTCT**C**AAATCACCCAACTTGCCATAGGTGACTCAGAACTCAAAAAAAACAAAGAAGAGGAGGATA	6922
	GGTGATTT**G**AGAATGTG	6923
	CACATTCT**C**AAATCACC	6924
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Glu8Term GAA-TAA	TCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAGTTGGGTGATTTCA**T**AATGTGGGCTAAGGCCACTTCCAAGAATCTATGCCAGGCCCAGAAGTGGAGCTTCATGTT	6925
	AACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGCCTTAGCCCACATT**A**TGAAATCACCCAACTTGCCATAGGTGACTCAGAACTCAAAAAAAACAAAGAAGAGGAGGA	6926
	TGATTTCA**T**AATGTGGG	6927
	CCCACATT**A**TGAAATCA	6928

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Cys9Term TGT-TGA	CTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAGTTGGGTGATTTCAGAATG**A**GGGCTAAGGCCACTTCCAAGAATCTATGCCAGGCCCAGAAGTGGAGCTTCATGTTTCAAC	6929
	GTTGAAACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGCCTTAGCCC**T**CATTCTGAAATCACCCAACTTGCCATAGGTGACTCAGAACTCAAAAAAAACAAAGAAGAG	6930
	TCAGAATG**A**GGGCTAAG	6931
	CTTAGCCC**T**CATTCTGA	6932
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Lys21Term AAA-TAA	ATGAAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTTTTCATGCT**T**AAGAAGAAGAAGAAGAAGAGGATTTCGACTTAAGCAATCCTCCTCCATTCAATATTGGTC	6933
	GACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTCTTCTTCTTCTTCTT**A**AGCATGAAAACCATTAACGCCATTTAGAATTGGGGTGTCTTTGTACTGTTGCTGCTTCAT	6934
	TTCATGCT**T**AAGAAGAA	6935
	TTCTTCTT**A**AGCATGAA	6936
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Glu22Term GAA-TAA	AAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTTTTCATGCTAAA**T**AAGAAGAAGAAGAAGAGGATTTCGACTTAAGCAATCCTCCTCCATTCAATATTGGTCAGA	6937
	TCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTCTTCTTCTTCTT**A**TTTAGCATGAAAACCATTAACGCCATTTAGAATTGGGGTGTCTTTGTACTGTTGCTGCTT	6938
	ATGCTAAA**T**AAGAAGAA	6939
	TTCTTCTT**A**TTTAGCAT	6940
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Glu23Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTTTTCATGCTAAAGAA**T**AAGAAGAAGAAGAGGATTTCGACTTAAGCAATCCTCCTCCATTCAATATTGGTCAGATCC	6941
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTCTTCTTCTT**A**TTCTTTAGCATGAAAACCATTAACGCCATTTAGAATTGGGGTGTCTTTGTACTGTTGCTG	6942
	CTAAAGAA**T**AAGAAGAA	6943
	TTCTTCTT**A**TTCTTTAG	6944
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Glu24Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTTTTCATGCTAAAGAA**T**AAGAAGAAGAAGAGGATTTCGACTTAAGCAATCCTCCTCCATTCAATATTGGTCAGATCC	6945
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTCTTCTTCTT**A**TTCTTTAGCATGAAAACCATTAACGCCATTTAGAATTGGGGTGTCTTTGTACTGTTGCTG	6946

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTAAAGAA**T**AAGAAGAA	6947
	TTCTTCTT**A**TTCTTTAG	6948
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Tyr21Term TAT-TAG	GGTCCAAGCACAGCCTCTACAACATGTTGGTAATGGTGCAGGGAA AGAAGATCAAGCTTA**G**TTTGATCCAAGTGCTCCACCACCCTTCAAG ATTGCAAATATCAGAGCAGCAATTCCAAAA	6949
	TTTTGGAATTGCTGCTCTGATATTTGCAATCTTGAAGGGTGGTGGA GCACTTGGATCAAA**C**TAAGCTTGATCTTCTTTCCCTGCACCATTAC CAACATGTTGTAGAGGCTGTGCTTGGACC	6950
	CAAGCTTA**G**TTTGATCC	6951
	GGATCAAA**C**TAAGCTTG	6952
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Lys31Term AAG-TAG	GGTAATGGTGCAGGGAAAGAAGATCAAGCTTATTTTGATCCAAGTG CTCCACCACCCTTC**T**AGATTGCAAATATCAGAGCAGCAATTCCAAA ACATTGCTGGGAGAAGAACACATTGAGAT	6953
	ATCTCAATGTGTTCTTCTCCCAGCAATGTTTTGGAATTGCTGCTCT GATATTTGCAATCT**A**GAAGGGTGGTGGAGCACTTGGATCAAAATAA GCTTGATCTTCTTTCCCTGCACCATTACC	6954
	CACCCTTC**T**AGATTGCA	6955
	TGCAATCT**A**GAAGGGTG	6956
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Arg36Term AGA-TGA	AAAGAAGATCAAGCTTATTTTGATCCAAGTGCTCCACCACCCTTCA AGATTGCAAATATC**T**GAGCAGCAATTCCAAAACATTGCTGGGAGAA GAACACATTGAGATCTCTGAGTTATGTTC	6957
	GAACATAACTCAGAGATCTCAATGTGTTCTTCTCCCAGCAATGTTTT GGAATTGCTGCTC**A**GATATTTGCAATCTTGAAGGGTGGTGGAGCA CTTGGATCAAAATAAGCTTGATCTTCTTT	6958
	CAAATATC**T**GAGCAGCA	6959
	TGCTGCTC**A**GATATTTG	6960
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Leu41Term AAA-TAA	TATTTTGATCCAAGTGCTCCACCACCCTTCAAGATTGCAAATATCA GAGCAGCAATTCCA**T**AACATTGCTGGGAGAAGAACACATTGAGATC TCTGAGTTATGTTCTGAGGGATGTGTTGG	6961
	CCAACACATCCCTCAGAACATAACTCAGAGATCTCAATGTGTTCTT CTCCCAGCAATGTT**A**TGGAATTGCTGCTCTGATATTTGCAATCTTG AAGGGTGGTGGAGCACTTGGATCAAAATA	6962
	CAATTCCA**T**AACATTGC	6963
	GCAATGTT**A**TGGAATTG	6964

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Glu8Term GAG-TAG	CATCCACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGGCTCGTGCTCTCC**T**AGTGCTCGGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGC	6965
	GCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGAGCACT**A**GGAGAGCACGAGCCGGGCCATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGGGTGGATG	6966
	TGCTCTCC**T**AGTGCTCG	6967
	CGAGCACT**A**GGAGAGCA	6968
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Cys9Term TGC-TGA	ACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGGCTCGTGCTCTCCGAGTG**A**TCGGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGCGGTCA	6969
	TGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGA**T**CACTCGGAGAGCACGAGCCGGGCCATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGGGT	6970
	TCCGAGTG**A**TCGGGCCT	6971
	AGGCCCGA**T**CACTCGGA	6972
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Ser10Term TCG-TAG	CCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGGCTCGTGCTCTCCGAGTGCT**A**GGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGCGGTCACC	6973
	GGTGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGGGCGCGAGGCCC**T**AGCACTCGGAGAGCACGAGCCGGGCCATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGG	6974
	CGAGTGCT**A**GGGCCTCG	6975
	CGAGGCCC**T**AGCACTCG	6976
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Ser29Term TCA-TGA	GCTCGGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGCGGT**G**ACCCCCCGCGCTCTCCGCGGCGCCGCGCCGTCGTCCCGCGTCCGCGTCCATCCACCGCGA	6977
	TCGCGGTGGATGGACGCGGACGCGGGACGACGGCGCGGCGCCGCGGAGAGCGCGGGGGGT**C**ACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGAGC	6978
	GGCGCGGT**G**ACCCCCCG	6979
	CGGGGGGT**C**ACCGCGCC	6980
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Glu8Term GAG-TAG	CCCCCTCCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCG**T**AGCAGGAGGCGAGCTGCAAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGC	6981
	GCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTTGCAGCTCGCCTCCTGCT**A**CGGCCTCATTGCGGGGGCCATGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGGAGGGGG	6982

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGAGGCCG**T**AGCAGGAG	6983
	CTCCTGCT**A**CGGCCTCA	6984
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Gln9Term CAG-TAG	CCTCCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCC CGCAATGAGGCCGGAG**T**AGGAGGCGAGCTGCAAGGCCACCGAG GACCACCGCTCCGAGTTCGACGCCGCCAAGCCGC	6985
	GCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGC CTTGCAGCTCGCCTCCT**A**CTCCGGCCTCATTGCGGGGGCCATGG CCGCGGATGGATCTGTGCGTGTGCGTGGGGGAGG	6986
	GGCCGGAG**T**AGGAGGCG	6987
	CGCCTCCT**A**CTCCGGCC	6988
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Glu10Term GAG-TAG	CCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGC AATGAGGCCGGAGCAG**T**AGGCGAGCTGCAAGGCCACCGAGGACC ACCGCTCCGAGTTCGACGCCGCCAAGCCGCCGC	6989
	GCGGCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGT GGCCTTGCAGCTCGCCT**A**CTGCTCCGGCCTCATTGCGGGGGCCA TGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGG	6990
	CGGAGCAG**T**AGGCGAGC	6991
	GCTCGCCT**A**CTGCTCCG	6992
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Cys13Term TGC-TGA	ACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGG AGCAGGAGGCGAGCTG**A**AAGGCCACCGAGGACCACCGCTCCGA GTTCGACGCCGCCAAGCCGCCGCCCTTCCGCATC	6993
	GATGCGGAAGGGCGGCGGCTTGGCGGCGTCGAACTCGGAGCGG TGGTCCTCGGTGGCCTT**T**CAGCTCGCCTCCTGCTCCGGCCTCATT GCGGGGGCCATGGCCGCGGATGGATCTGTGCGT	6994
	GCGAGCTG**A**AAGGCCAC	6995
	GTGGCCTT**T**CAGCTCGC	6996
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Ser4Term TCG-TAG	CTTCACAAATCACAAATCGGAATCAGATCCACCACGACACCCCGG CGGCAATGGCGGCGT**A**GGCGACCCAGGAGGCCGACTGCAAGGC TTCCGAGGACGCCCGTCTCTTCTTCGACGCCGC	6997
	GCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGCCTTGCAGTC GGCCTCCTGGGTCGCC**T**ACGCCGCCATTGCCGCCGGGGTGTCGT GGTGGATCTGATTCCGATTTGTGATTTGTGAAG	6998
	GGCGGCGT**A**GGCGACCC	6999
	GGGTCGCC**T**ACGCCGCC	7000

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Gln7Term CAG-TAG	ATCACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATG GCGGCGTCGGCGACC**T**AGGAGGCCGACTGCAAGGCTTCCGAGG ACGCCCGTCTCTTCTTCGACGCCGCCAAGCCCC	7001
	GGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGC CTTGCAGTCGGCCTCCT**A**GGTCGCCGACGCCGCCATTGCCGCCG GGGTGTCGTGGTGGATCTGATTCCGATTTGTGAT	7002
	CGGCGACC**T**AGGAGGCC	7003
	GGCCTCCT**A**GGTCGCCG	7004
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Glu8Term GAG-TAG	ACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATGGC GGCGTCGGCGACCCAG**T**AGGCCGACTGCAAGGCTTCCGAGGACG CCCGTCTCTTCTTCGACGCCGCCAAGCCCCCGC	7005
	GCGGGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGA AGCCTTGCAGTCGGCCT**A**CTGGGTCGCCGACGCCGCCATTGCCG CCGGGGTGTCGTGGTGGATCTGATTCCGATTTGT	7006
	CGACCCAG**T**AGGCCGAC	7007
	GTCGGCCT**A**CTGGGTCG	7008
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Cys10Term TGC-TGA	TCAGATCCACCACGACACCCCGGCGGCAATGGCGGCGTCGGCGA CCCAGGAGGCCGACTG**A**AAGGCTTCCGAGGACGCCCGTCTCTTC TTCGACGCCGCCAAGCCCCCGCCCTTCCGCATC	7009
	GATGCGGAAGGGCGGGGGCTTGGCGGCGTCGAAGAAGAGACGG GCGTCCTCGGAAGCCTT**T**CAGTCGGCCTCCTGGGTCGCCGACGC CGCCATTGCCGCCGGGGTGTCGTGGTGGATCTGA	7010
	GCCGACTG**A**AAGGCTTC	7011
	GAAGCCTT**T**CAGTCGGC	7012

WHAT IS CLAIMED IS:

1. An oligonucleotide for targeted alteration of genetic sequence, comprising a single-stranded oligonucleotide having a DNA domain, said DNA domain having at least one mismatch with respect to the genetic sequence to be altered, and further comprising chemical modifications of the oligonucleotide, said chemical modifications selected from the group consisting of an o-methyl modification, an LNA modification including LNA derivatives and analogs, two or more phosphorothioate linkages on a terminus, and a combination of any two or more of these modifications.

2. The oligonucleotide according to claim one that comprises two or more phosphorothioate linkages on at least the 3' terminus.

3. The oligonucleotide according to claim one that comprises a 2'-O-methyl analog.

4. The oligonucleotide according to claim one that comprises an LNA nucleotide, including an LNA derivative or analog.

5. The oligonucleotide according to claim one that comprises a combination of at least two modifications selected from the group of a phosphorothioate linkage, a 2'-O-methyl analog, a locked nucleotide analog and a ribonucleotide.

6. The oligonucleotide according to any one of claims 1 to 5 that comprises at least one unmodified ribonucleotide.

7. The oligonucleotide according to any one of claims 1 to 6, wherein the sequence of said oligonucleotide is selected from the group consisting of SEQ ID NOS: 4341-7012 .

8. A method of targeted alteration of genetic material, comprising combining the target genetic material with an oligonucleotide according to any one of claims 1 to 7 in the presence of purified proteins.

9. A method of targeted alteration of genetic material, comprising administering to a cell extract an oligonucleotide of any one of claims 1 to 7.

10. A method of targeted alteration of genetic material, comprising administering to a cell an oligonucleotide of any one of claims 1 to 7.

11. A method of targeted alteration of genetic sequence in callus, comprising administering to the callus an oligonucleotide of any one of claims 1 to 7.

12. A method of targeted alteration of genetic sequence, comprising combining target genetic material with an oligonucleotide according to any one of claims 1 to 7, said target genetic material being a non-transcribed DNA strand of a duplex DNA.

13. The genetic material obtained by any one of the methods of claim 8, 9 or claim 10.

14. A cell comprising the genetic material of claim 13.

15. A plant organism comprising the cell according to claim 14.

16. A plant or plant part produced by the method of claim 11.

17. A method of determining whether an oligonucleotide is optimized for targeted alteration of a genetic sequence, which comprises:

(a) comparing the efficiency of alteration of a targeted genetic sequence by an oligonucleotide of any one of claims 1 to 7 with the efficiency of alteration of the same targeted genetic sequence by a second oligonucleotide, said second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2'-O-methylated oligonucleotide and a chimeric double-stranded double hairpin containing RNA and DNA nucleotides.

18. The method of claim 17 in which the alteration is produced in a plant cell extract.

19. The method of claim 17 in which the alteration is produced in a cell.

20. A kit comprising the oligonucleotide according to any one of claims 1 to 7 and a second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2-O-methylated oligonucleotide and a chimeric double stranded double hairpin containing RNA and DNA nucleotides.

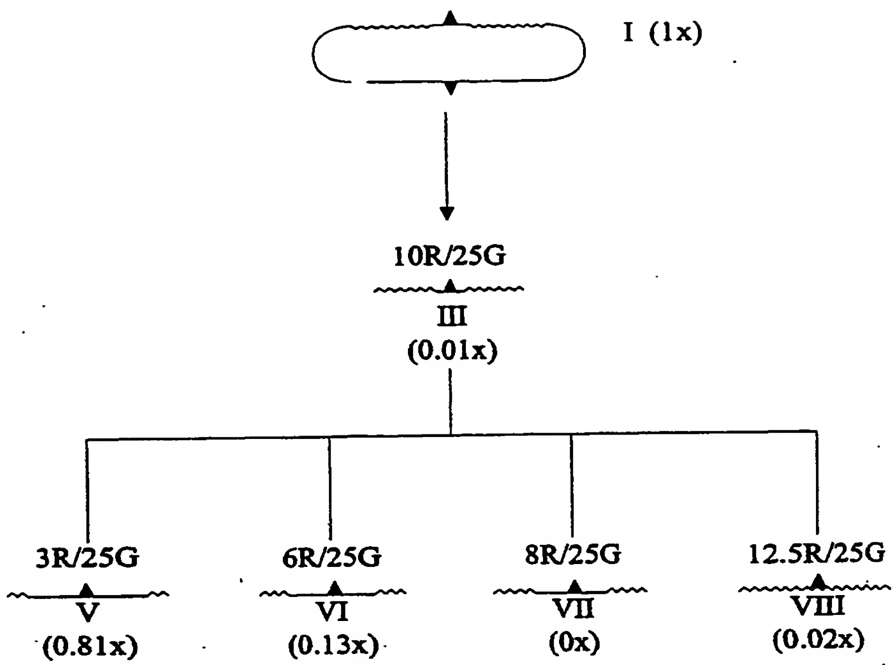


Figure 1A

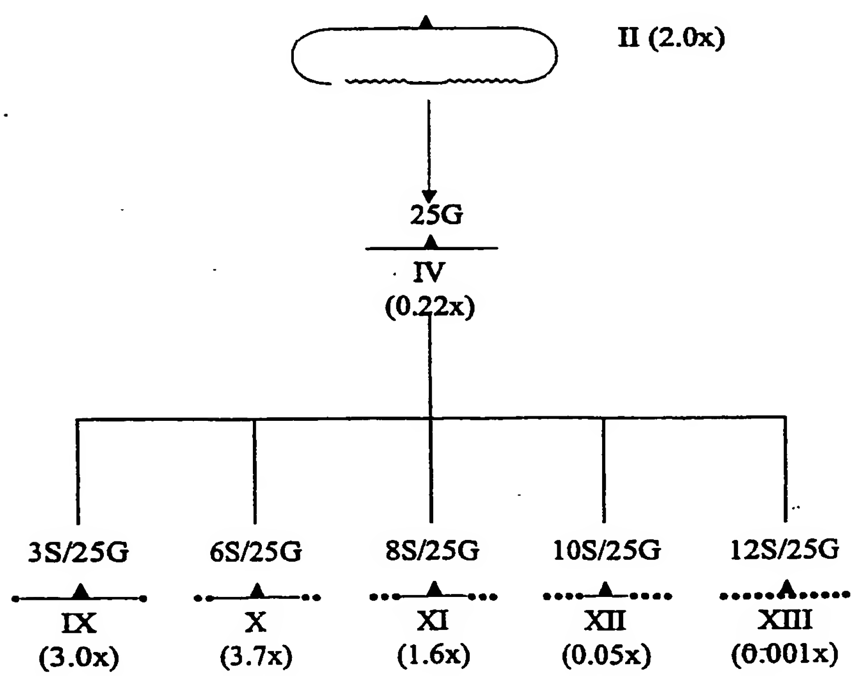


Figure 1B

Plasmids, DNA targets and chimeric oligonucleotides

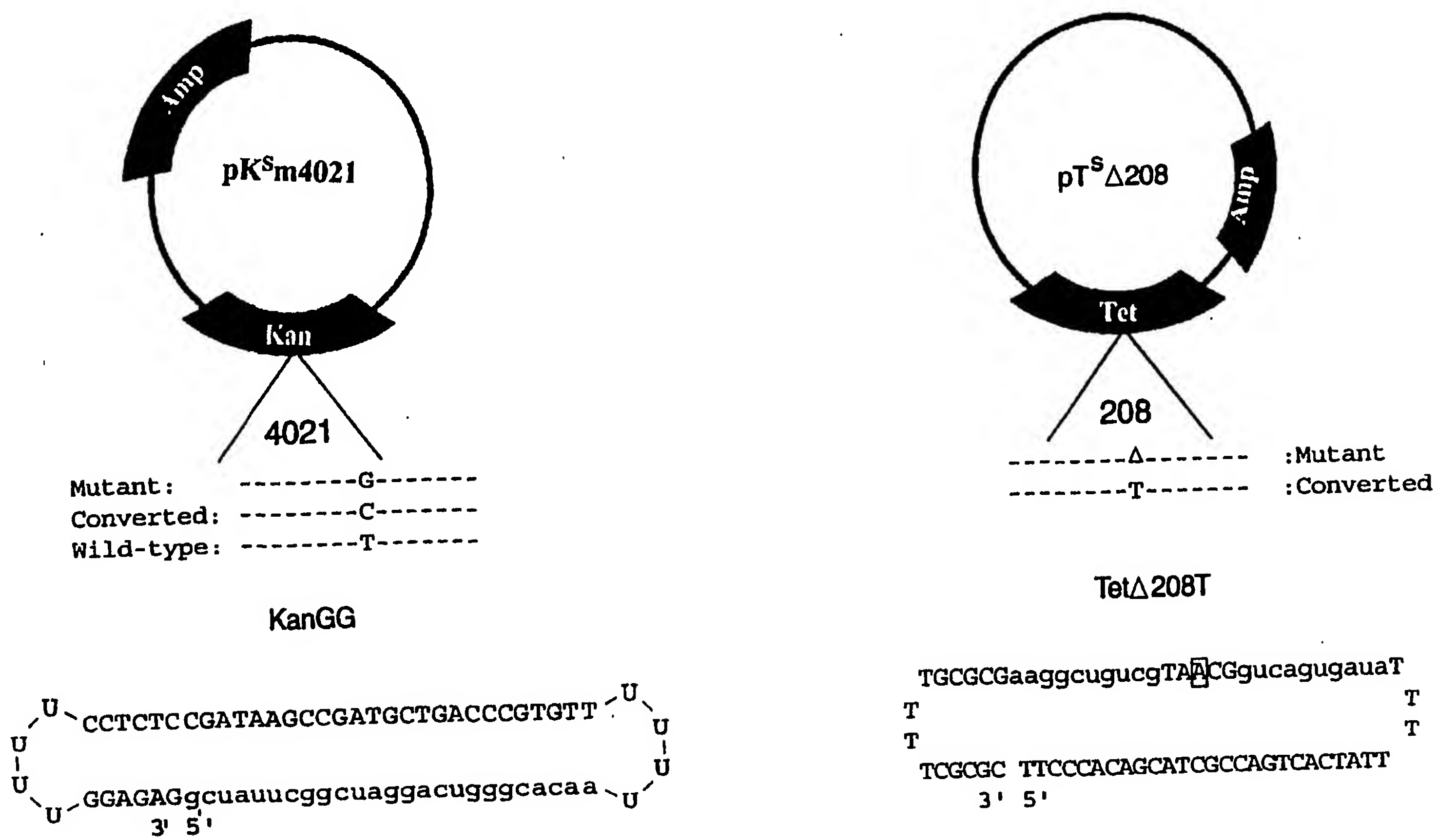


Figure 1C

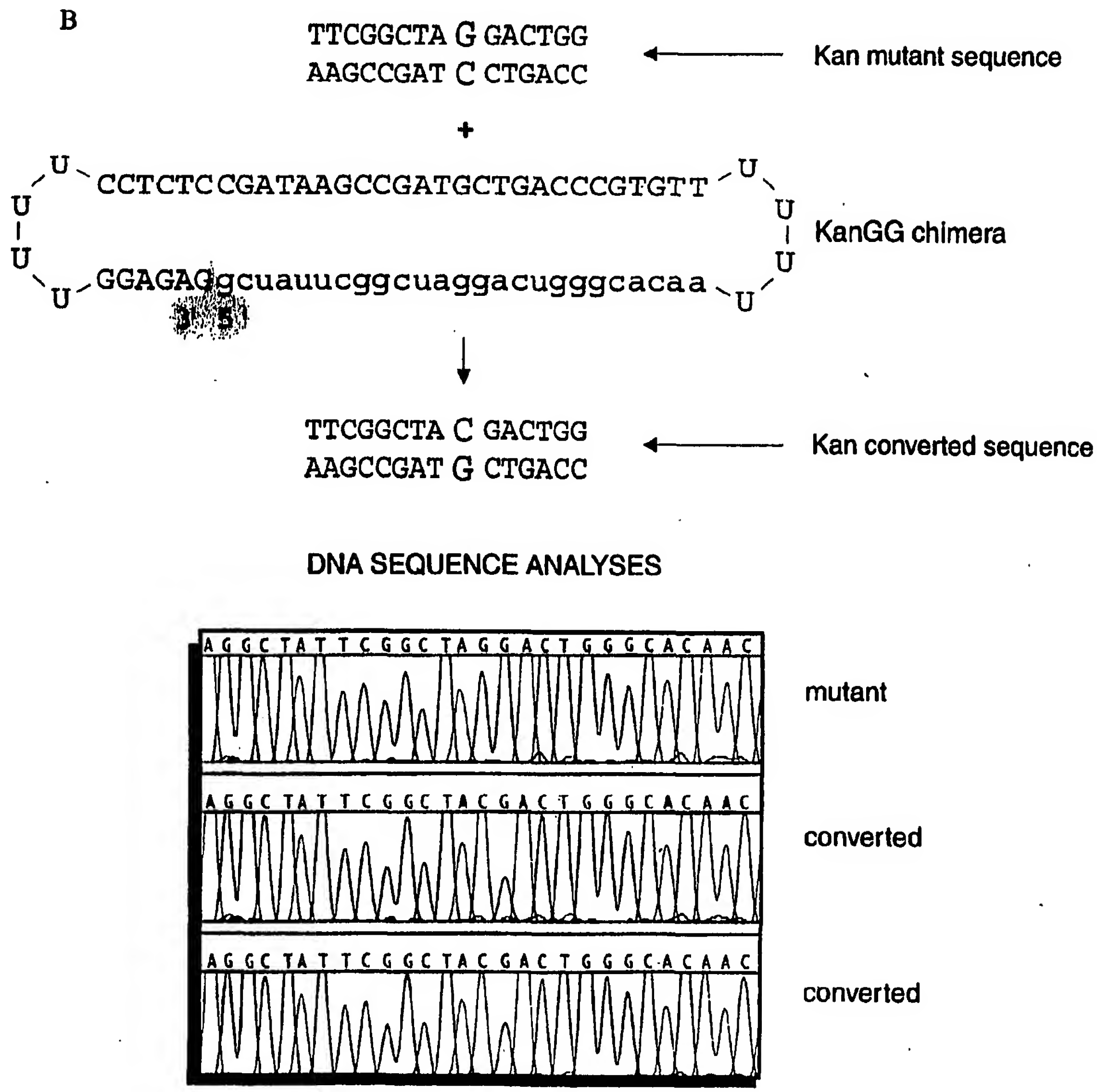

B
TTCGGCTA G GACTGG
AAGCCGAT C CTGACC
Kan mutant sequence
+
CCTCTCCGATAAGCCGATGCTGACCCGTGTT
GGAGAGgcuauucggcuaggacugggcacaa
U U U U U U U U
KanGG chimera
TTCGGCTA C GACTGG
AAGCCGAT G CTGACC
Kan converted sequence
DNA SEQUENCE ANALYSES
AGGCTATTCGGCTAGGACTGGGCACAAC
mutant
AGGCTATTCGGCTACGACTGGGCACAAC
converted
AGGCTATTCGGCTACGACTGGGCACAAC
converted

Figure 1D

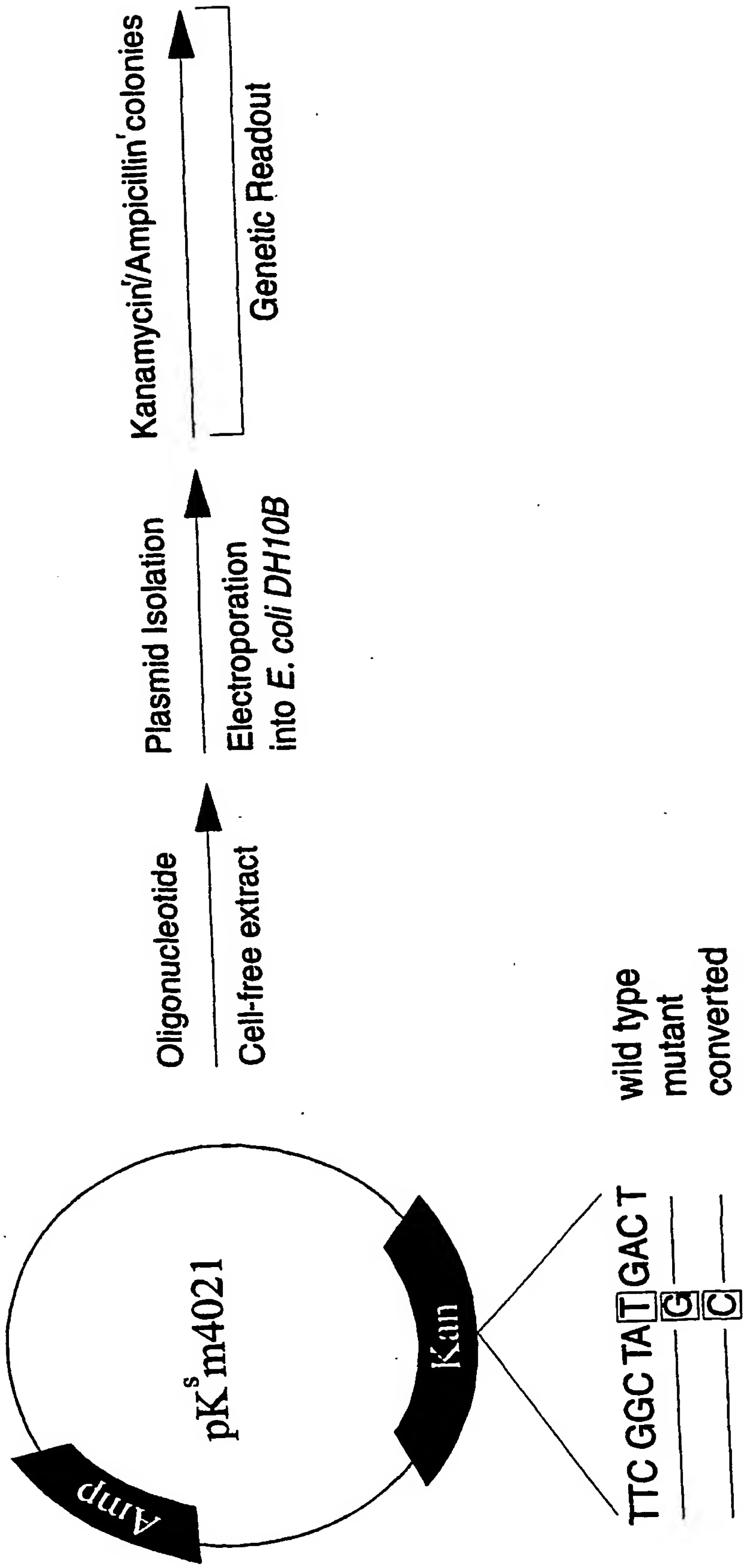
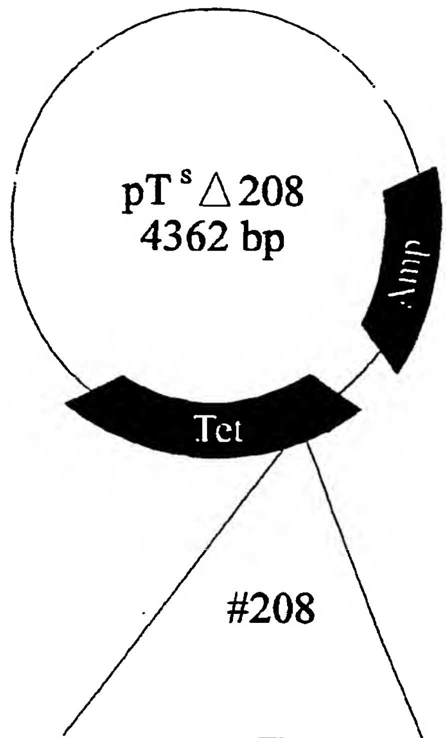

pK^{s}m4021
Amp
Kan
TTC GGC TA T GAC T
G
C
wild type
mutant
converted
Oligonucleotide
Cell-free extract
Plasmid Isolation
Electroporation into E. coli DH10B
Kanamycin^r/Ampicillin^r colonies
Genetic Readout

Figure 2



Wild type: GAC AGC AT $\boxed{C}$ GCCAGT
Mutant: GAC AGC AT - GCCAGT
Converted: GAC AGC AT $\boxed{T}$ GCCAGT

Sequence analysis of Tet[r] plasmid △208

Control

3S/25A

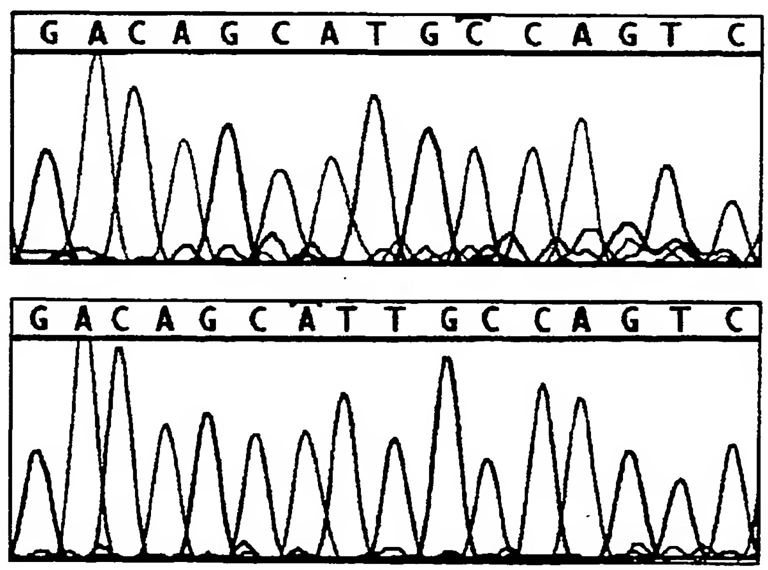


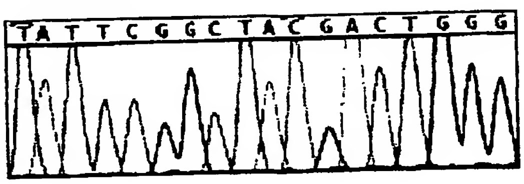
Figure 3

DNA sequence analysis of Kan^r plasmids

Target codon distribution

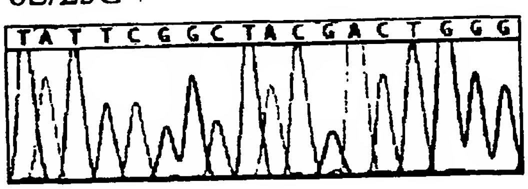
oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)	—	+	—	—	—
2) 6S/25G (20)	—	+	—	—	—
3) 8S/25G (20)	—	+	—	—	—
4) 10S/25G (18)	—	+	—	+(2)	+(2)
5) 25S/25G (4)	—	—	+(2)	+(2)	—

3S/25G

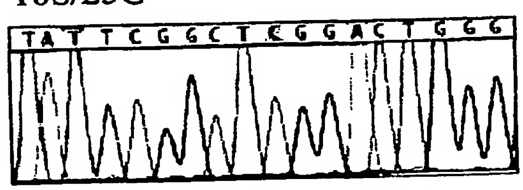


6S/25G

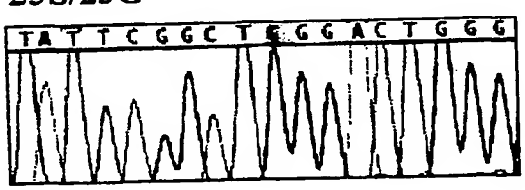
8S/25G



10S/25G



25S/25G



25S/25G

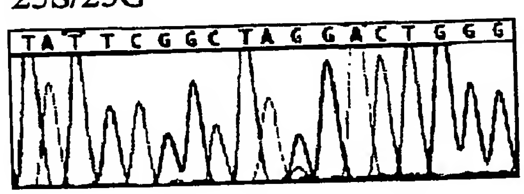


Figure 4

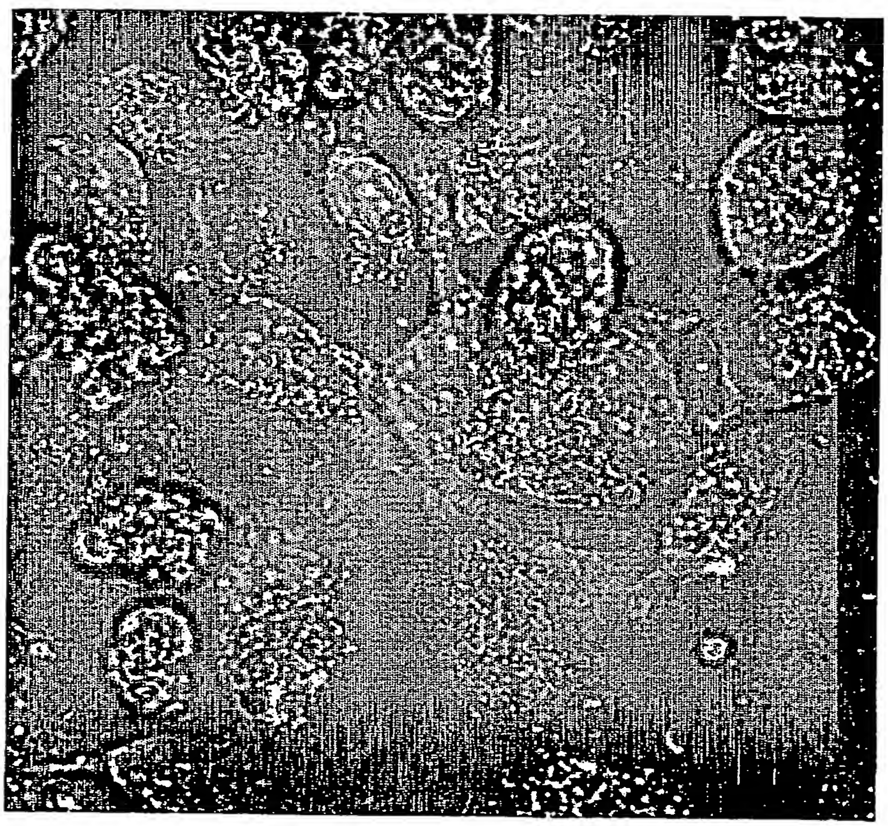


Figure 5

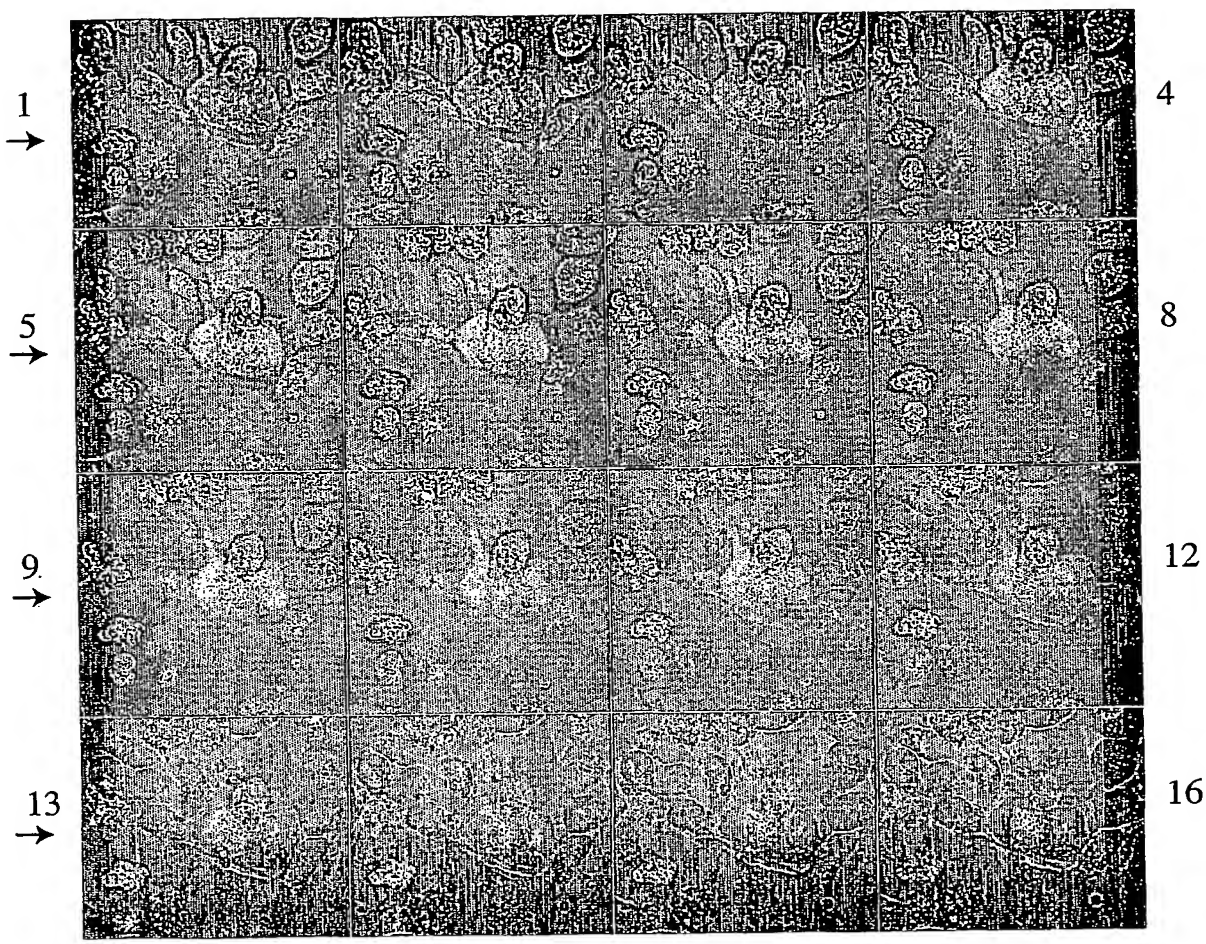
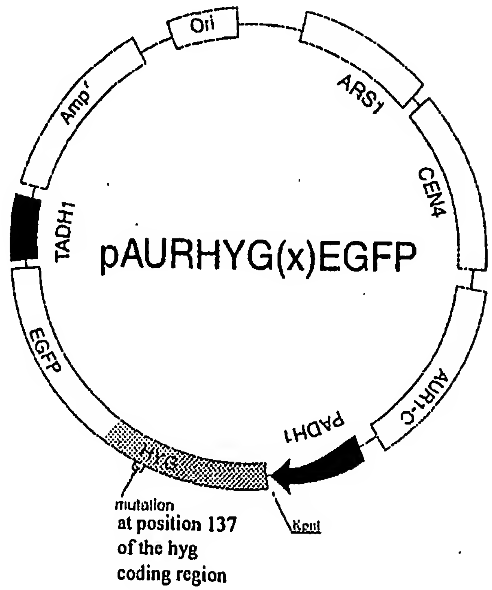


Figure 6



Sequence of normal allele:	GTGGATATGTCCT
Target/existing mutant:	GTGGATAATGTCCT
Desired alteration:	GTGGATACGTCCT

Figure 7A

Sequence of normal allele:	GTGGATATGTCCT
Target/existing mutant:	GTGGATAGGTCCT
Desired alteration:	GTGGATACGTCCT

Figure 7B

HygE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

HygE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG CCG ATG GTT TCT AC-3'

HygE3T/74α: 5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA GCT GAA AGC ACG AG-3'

HygGG/Rev:

```
  T                                   T
 / \                                 / \
T   ACATCCTCCCGCACCTATGCAGGACGCCCAT   T
T   TGTAGGagggcguggaTAGGTccugcgggua   T
 \ /       / \                       \ /
  T      3'   5'                      T
```

Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG A-3'

Figure 8

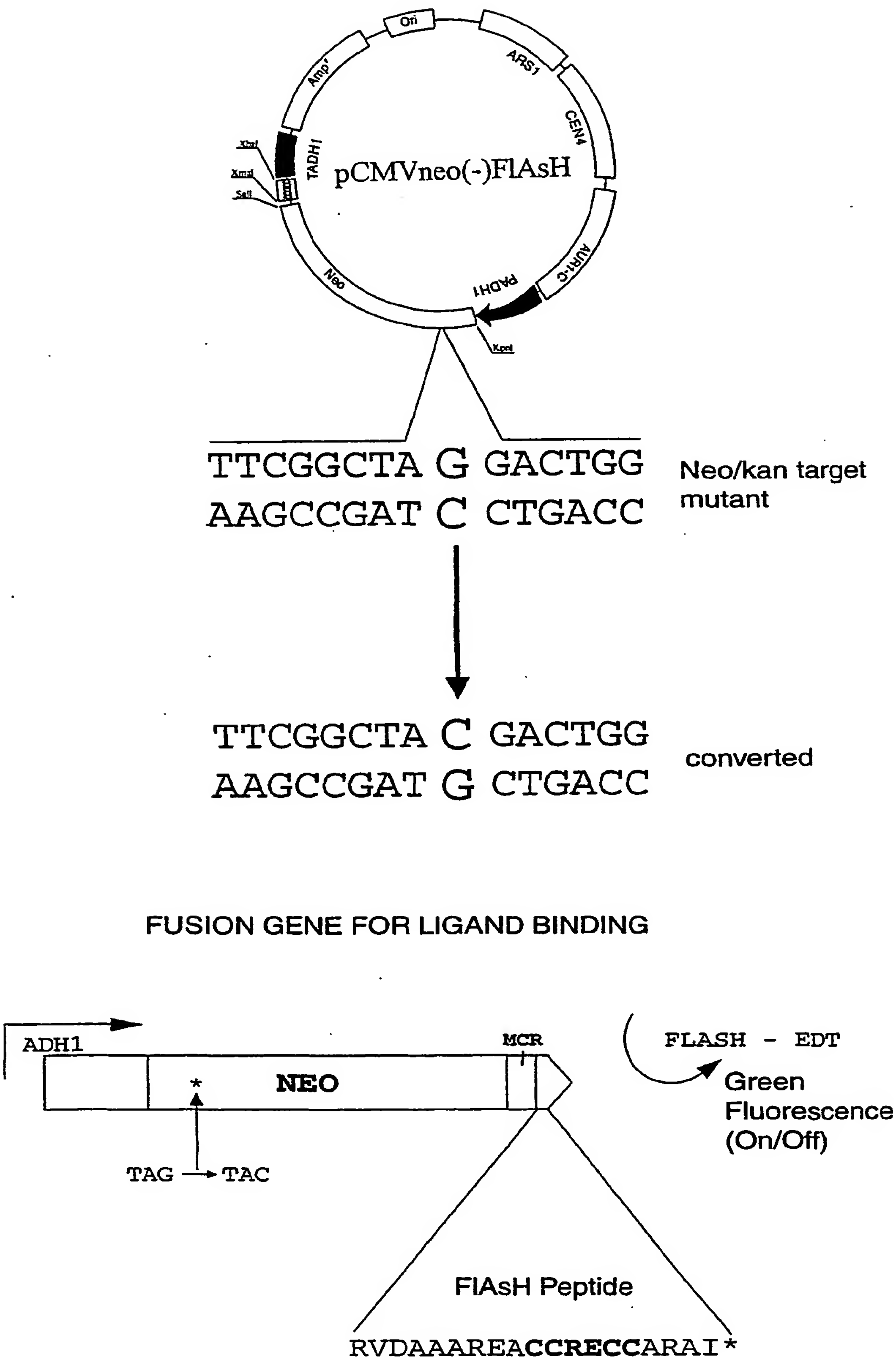

Ori
ARS1
CEN4
AUR1-C
PADH1
KpnI
Neo
SalI
XmaI
XhoI
TADH1
Ampr
pCMVneo(-)FlAsH
TTCGGCTA G GACTGG
AAGCCGAT C CTGACC
Neo/kan target mutant
TTCGGCTA C GACTGG
AAGCCGAT G CTGACC
converted
FUSION GENE FOR LIGAND BINDING
ADH1
NEO
*
MCR
TAG → TAC
FLASH - EDT
Green Fluorescence (On/Off)
FlAsH Peptide
RVDAAAREACCRECCARAI*

Figure 9

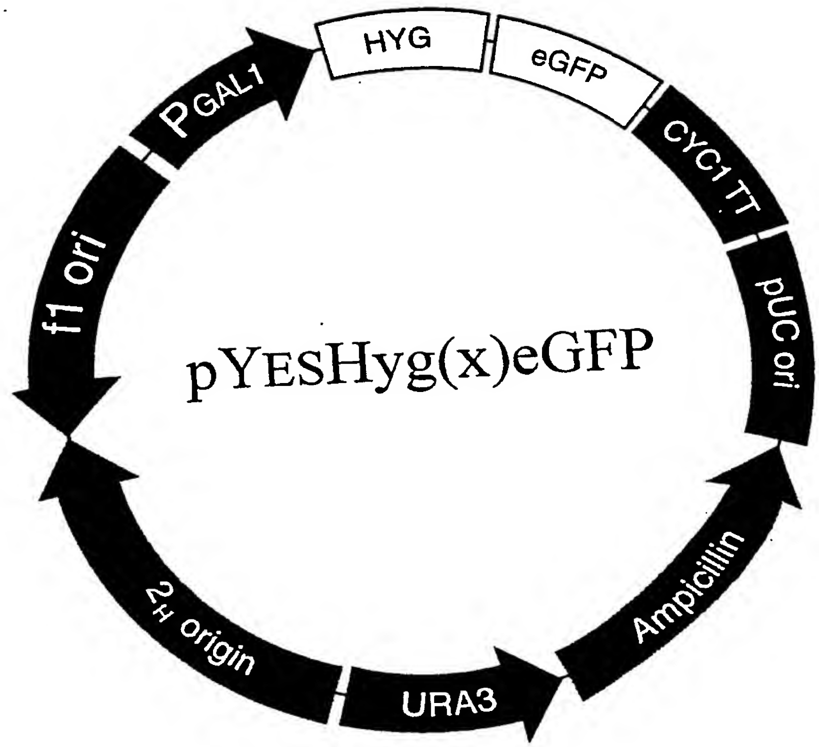

HYG
eGFP
CYC1 TT
pUC ori
Ampicillin
URA3
2μ origin
f1 ori
PGAL1
pYESHyg(x)eGFP

Figure 10

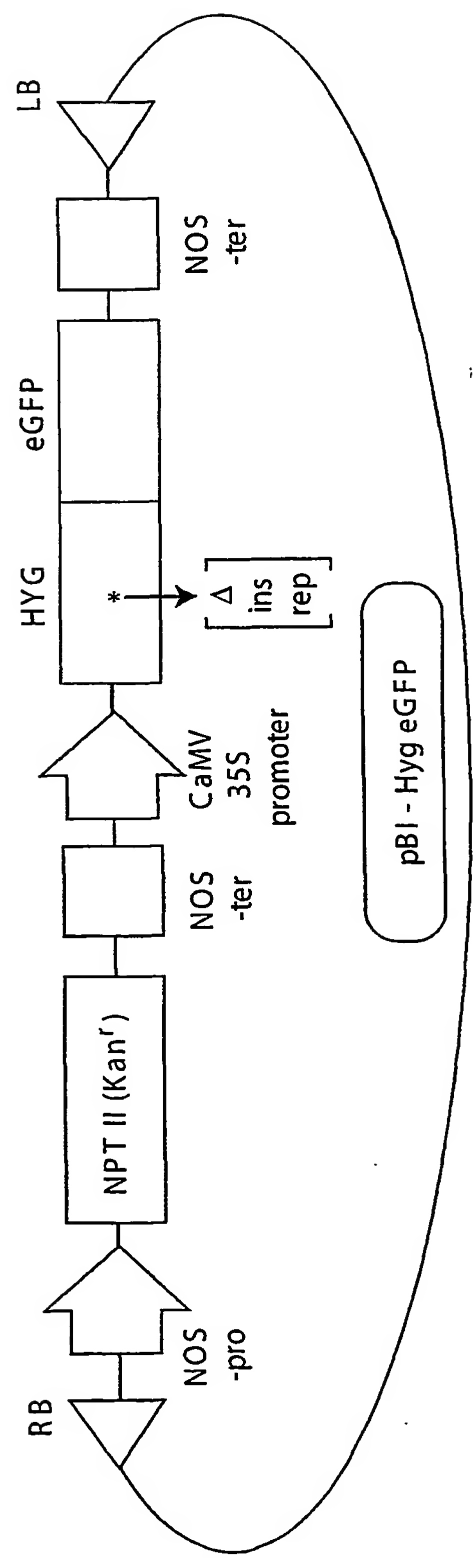

LB
NOS
-ter
eGFP
HYG
*
Δ
ins
rep
CaMV
35S
promoter
NOS
-ter
NPT II (Kan^r)
NOS
-pro
RB
pBI - Hyg eGFP

Figure 11

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
6 December 2001 (06.12.2001)

PCT

(10) International Publication Number
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(51) International Patent Classification⁷: C12N 15/10, 15/82, 15/11, C07H 21/04, A61K 31/7088, C12N 5/04, A01H 5/00

(21) International Application Number: PCT/US01/17672

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60/244,989	30 October 2000 (30.10.2000)	US
09/818,875	27 March 2001 (27.03.2001)	US

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(72) **Inventors; and**
(75) **Inventors/Applicants** *(for US only)*: **KMIEC, Eric, B.** [US/US]; 18 Crossan Court, Landenberg, PA 19350 (US). **GAMPER, Howard, B.** [US/US]; 904 Locust Street, Philadelphia, PA 19107 (US). **RICE, Michael, C.** [US/US]; 802 Washington Crossing Road, Newtown, PA 18940 (US). **KIM, Jungsup** [KR/US]; 3 Chase Hall, Newark, DE 19711 (US).

(74) **Agents: HALEY, James, F., Jr.** et al.; Fish & Neave, 1251 Avenue of the Americas, New York, NY 10020 (US).

(81) **Designated States** *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) **Designated States** *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

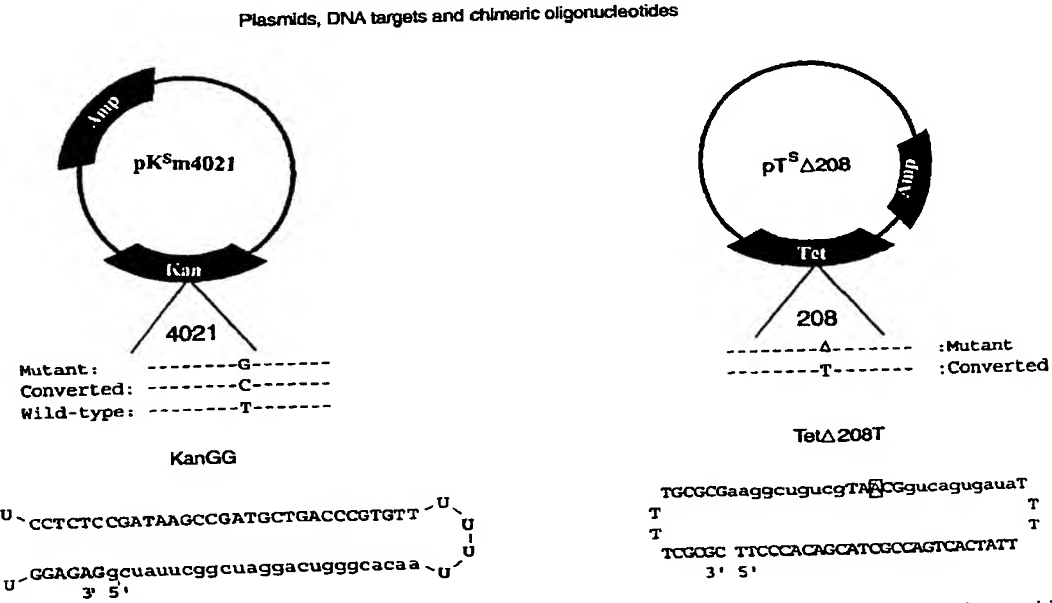
Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA,*

[Continued on next page]

(54) **Title:** TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

Plasmids, DNA targets and chimeric oligonucleotides



(57) **Abstract:** Presented are methods and compositions for targeted chromosomal genomic alterations with modified single-stranded oligonucleotides. The oligonucleotides of the invention have modified nuclease-resisant termini comprising LNA, phosphorothioate linkages or 2'-O-Me base analogues or combinations of such modifications.

WO 01/092512 A3

CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG)

— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG)*

— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG)*

— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG)*

Published:

— *with international search report*

(88) Date of publication of the international search report: 9 January 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/17672

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/10 C12N15/82 C12N15/11 C07H21/04 A61K31/7088
C12N5/04 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WOOLF T M ET AL: "TOWARD THE THERAPEUTIC EDITING OF MUTATED RNA SEQUENCES" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 92, 1 August 1995 (1995-08-01), pages 8298-8302, XP000574995 ISSN: 0027-8424	1-3,5,8, 9,12-14, 17,20
Y	the whole document	1-6, 8-12,17, 18,20

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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"&" document member of the same patent family

Date of the actual completion of the international search

22 March 2002

Date of mailing of the international search report

23. 07. 2002

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Fax: (+31-70) 340-3016

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ANDRES S.M.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/17672

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X Y	GAMPER HOWARD B JR ET AL: "A plausible mechanism for gene correction by chimeric oligonucleotides." BIOCHEMISTRY, vol. 39, no. 19, 16 May 2000 (2000-05-16), pages 5808-5816, XP002192327 ISSN: 0006-2960 cited in the application the whole document ---	13-16 1-6,8-12
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P,X	WO 01 15740 A (VALIGEN US INC) 8 March 2001 (2001-03-08) the whole document --- -/--	1-6,8-16

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/17672

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,A	WO 01 24615 A (VALIGEN US INC) 12 April 2001 (2001-04-12) the whole document ---	1-20
E	WO 01 73002 A (UNIV DELAWARE ;GAMPER HOWARD B (US); KMIEC ERIC B (US); RICE MICHA) 4 October 2001 (2001-10-04) the whole document ---	1-6,8-20
T	RICE MICHAEL C ET AL: "The potential of nucleic acid repair in functional genomics." NATURE BIOTECHNOLOGY, vol. 19, no. 4, April 2001 (2001-04), pages 321-326, XP002192330 ISSN: 1087-0156 ---	
T	KMIEC ERIC B ET AL: "Chloroplast lysates support directed mutagenesis via modified DNA and chimeric RNA/DNA oligonucleotides." PLANT JOURNAL, vol. 27, no. 3, August 2001 (2001-08), pages 267-274, XP002192584 ISSN: 0960-7412 -----	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/17672

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 8,10,12 (as far as in vivo methods) are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 (all partially)

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. : Claims 1-20 (all partially)

Oligonucleotides characterised by SEQ IDs 4341-4344 for targeted alteration of the Arabidopsis EPSPS at aminoacid position 97; modified forms thereof; compositions and kits comprising them; methods for their optimisation.

Inventions 2. to 668. : Claims 1-20 (all partially)

As for subject 1., but concerning respectively the 667 groups of altering oligonucleotides (SEQ IDs 4345-7012) for each individual mutation disclosed in Tables 10 to 24.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/US 01/17672

Patent document cited in search report		Publication date	Patent family member(s)			Publication date
WO 9907865	A	18-02-1999	AU	748015	B2	30-05-2002
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			DE	3850527	T2	22-12-1994
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			CN	1279687	T	10-01-2001
			WO	9914226	A2	25-03-1999
			EP	1015469	A2	05-07-2000
			NZ	503765	A	26-04-2002
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			AU	7076700	A	26-03-2001
			BR	0013590	A	07-05-2002
			EP	1210123	A1	05-06-2002
			WO	0115740	A1	08-03-2001
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			WO	0124615	A1	12-04-2001
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